

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
27 December 2001 (27.12.2001)

PCT

(10) International Publication Number
WO 01/98468 A2

(51) International Patent Classification⁷: C12N 9/00

(21) International Application Number: PCT/US01/19178

(22) International Filing Date: 13 June 2001 (13.06.2001)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/212,336	16 June 2000 (16.06.2000)	US
60/213,955	22 June 2000 (22.06.2000)	US
60/215,396	29 June 2000 (29.06.2000)	US
60/216,821	7 July 2000 (07.07.2000)	US
60/218,946	14 July 2000 (14.07.2000)	US

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(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: PROTEASES

(57) Abstract: The invention provides human proteases (PRTS) and polynucleotides which identify and encode PRTS. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders associated with aberrant expression of PRTS.

PROTEASES

TECHNICAL FIELD

This invention relates to nucleic acid and amino acid sequences of proteases and to the use of these sequences in hydrolysis of peptide bonds and in the diagnosis, treatment, and prevention of gastrointestinal, cardiovascular, autoimmune/inflammatory, cell proliferative, developmental, epithelial, neurological, and reproductive disorders, and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of proteases.

BACKGROUND OF THE INVENTION

Proteases cleave proteins and peptides at the peptide bond that forms the backbone of the protein or peptide chain. Proteolysis is one of the most important and frequent enzymatic reactions that occurs both within and outside of cells. Proteolysis is responsible for the activation and maturation of nascent polypeptides, the degradation of misfolded and damaged proteins, and the controlled turnover of peptides within the cell. Proteases participate in digestion, endocrine function, and tissue remodeling during embryonic development, wound healing, and normal growth. Proteases can play a role in regulatory processes by affecting the half life of regulatory proteins. Proteases are involved in the etiology or progression of disease states such as inflammation, angiogenesis, tumor dispersion and metastasis, cardiovascular disease, neurological disease, and bacterial, parasitic, and viral infections.

Proteases can be categorized on the basis of where they cleave their substrates. Exopeptidases, which include aminopeptidases, dipeptidyl peptidases, tripeptidases, carboxypeptidases, peptidyl-dipeptidases, dipeptidases, and omega peptidases, cleave residues at the termini of their substrates. Endopeptidases, including serine proteases, cysteine proteases, and metalloproteases, cleave at residues within the peptide. Four principal categories of mammalian proteases have been identified based on active site structure, mechanism of action, and overall three-dimensional structure. (See Beynon, R.J. and J.S. Bond (1994) Proteolytic Enzymes: A Practical Approach, Oxford University Press, New York NY, pp. 1-5.)

Serine Proteases

The serine proteases (SPs) are a large, widespread family of proteolytic enzymes that include the digestive enzymes trypsin and chymotrypsin, components of the complement and blood-clotting cascades, and enzymes that control the degradation and turnover of macromolecules within the cell and in the extracellular matrix. Most of the more than 20 subfamilies can be grouped into six clans, each with a common ancestor. These six clans are hypothesized to have descended from at least four evolutionarily distinct ancestors. SPs are named for the presence of a serine residue found in the active

catalytic site of most families. The active site is defined by the catalytic triad, a set of conserved asparagine, histidine, and serine residues critical for catalysis. These residues form a charge relay network that facilitates substrate binding. Other residues outside the active site form an oxyanion hole that stabilizes the tetrahedral transition intermediate formed during catalysis. SPs have a wide range of substrates and can be subdivided into subfamilies on the basis of their substrate specificity. The main subfamilies are named for the residue(s) after which they cleave: trypases (after arginine or lysine), aspases (after aspartate), chymases (after phenylalanine or leucine), metases (methionine), and serases (after serine) (Rawlings, N.D. and A.J. Barrett (1994) *Methods Enzymol.* 244:19-61).

Most mammalian serine proteases are synthesized as zymogens, inactive precursors that are activated by proteolysis. For example, trypsinogen is converted to its active form, trypsin, by enteropeptidase. Enteropeptidase is an intestinal protease that removes an N-terminal fragment from trypsinogen. The remaining active fragment is trypsin, which in turn activates the precursors of the other pancreatic enzymes. Likewise, proteolysis of prothrombin, the precursor of thrombin, generates three separate polypeptide fragments. The N-terminal fragment is released while the other two fragments, which comprise active thrombin, remain associated through disulfide bonds.

The two largest SP subfamilies are the chymotrypsin (S1) and subtilisin (S8) families. Some members of the chymotrypsin family contain two structural domains unique to this family. Kringle domains are triple-looped, disulfide cross-linked domains found in varying copy number. Kringles are thought to play a role in binding mediators such as membranes, other proteins or phospholipids, and in the regulation of proteolytic activity (PROSITE PDOC00020). Apple domains are 90 amino-acid repeated domains, each containing six conserved cysteines. Three disulfide bonds link the first and sixth, second and fifth, and third and fourth cysteines (PROSITE PDOC00376). Apple domains are involved in protein-protein interactions. S1 family members include trypsin, chymotrypsin, coagulation factors IX-XII, complement factors B, C, and D, granzymes, kallikrein, and tissue- and urokinase-plasminogen activators. The subtilisin family has members found in the eubacteria, archaeobacteria, eukaryotes, and viruses. Subtilisins include the proprotein-processing endopeptidases kexin and furin and the pituitary prohormone convertases PC1, PC2, PC3, PC6, and PACE4 (Rawlings and Barrett, *supra*). The prolyl oligopeptidase (S9) family includes enzymes from prokaryotes and eukaryotes with greatly differing specificities. Dipeptidyl peptidase IV (DPP-IV) is identical to CD26 and is implicated in the inactivation of peptide hormones, as well as in regulating T-cell growth (reviewed in Kahne, T. et al. (1999) *Int. J. Mol. Med.* 4:3-15; Mentlein, R. (1999) *Regul. Pept.* 85:9-24). Inhibition of DPP-IV has been suggested as a treatment for type 2 diabetes (Holst, J.J. and C.F. Deacon (1998) *Diabetes* 47:1663-1670), and lowered serum DPP-IV activity has been measured in anorexia and bulimia patients (van West, D. et al. (2000) *Eur. Arch. Psych. Clin. Neurosci.* 250:86-92).

SPs have functions in many normal processes and some have been implicated in the etiology or treatment of disease. Enterokinase, the initiator of intestinal digestion, is found in the intestinal brush border, where it cleaves the acidic propeptide from trypsinogen to yield active trypsin (Kitamoto, Y. et al. (1994) *Proc. Natl. Acad. Sci. USA* 91:7588-7592). Prolylcarboxypeptidase, a lysosomal serine
5 peptidase that cleaves peptides such as angiotensin II and III and [des-Arg9] bradykinin, shares sequence homology with members of both the serine carboxypeptidase and prolylendopeptidase families (Tan, F. et al. (1993) *J. Biol. Chem.* 268:16631-16638). The protease neuropsin may influence synapse formation and neuronal connectivity in the hippocampus in response to neural signaling (Chen, Z.-L. et al. (1995) *J. Neurosci.* 15:5088-5097). Tissue plasminogen activator is useful for acute
10 management of stroke (Zivin, J.A. (1999) *Neurology* 53:14-19) and myocardial infarction (Ross, A.M. (1999) *Clin. Cardiol.* 22:165-171). Some receptors (PAR, for proteinase-activated receptor), highly expressed throughout the digestive tract, are activated by proteolytic cleavage of an extracellular domain. The major agonists for PARs, thrombin, trypsin, and mast cell tryptase, are released in allergy and inflammatory conditions. Control of PAR activation by proteases has been suggested as a
15 promising therapeutic target (Vergnolle, N. (2000) *Aliment. Pharmacol. Ther.* 14:257-266; Rice, K.D. et al. (1998) *Curr. Pharm. Des.* 4:381-396). Prostate-specific antigen (PSA) is a kallikrein-like serine protease synthesized and secreted exclusively by epithelial cells in the prostate gland. Serum PSA is elevated in prostate cancer and is the most sensitive physiological marker for monitoring cancer progression and response to therapy. PSA can also identify the prostate as the origin of a metastatic
20 tumor (Brawer, M.K. and P.H. Lange (1989) *Urology* 33:11-16).

The signal peptidase is a specialized class of SP found in all prokaryotic and eukaryotic cell types that serves in the processing of signal peptides from certain proteins. Signal peptides are amino-terminal domains of a protein which direct the protein from its ribosomal assembly site to a particular cellular or extracellular location. Once the protein has been exported, removal of the signal
25 sequence by a signal peptidase and posttranslational processing, e.g., glycosylation or phosphorylation, activate the protein. Signal peptidases exist as multi-subunit complexes in both yeast and mammals. The canine signal peptidase complex is composed of five subunits, all associated with the microsomal membrane and containing hydrophobic regions that span the membrane one or more times (Shelness, G.S. and G. Blobel (1990) *J. Biol. Chem.* 265:9512-9519). Some of these subunits serve to fix the
30 complex in its proper position on the membrane while others contain the actual catalytic activity.

Another family of proteases which have a serine in their active site are dependent on the hydrolysis of ATP for their activity. These proteases contain proteolytic core domains and regulatory ATPase domains which can be identified by the presence of the P-loop, an ATP/GTP-binding motif (PROSITE PDOC00803). Members of this family include the eukaryotic mitochondrial matrix

proteases, Clp protease and the proteasome. Clp protease was originally found in plant chloroplasts but is believed to be widespread in both prokaryotic and eukaryotic cells. The gene for early-onset torsion dystonia encodes a protein related to Clp protease (Ozelius, L.J. et al. (1998) *Adv. Neurol.* 78:93-105).

The proteasome is an intracellular protease complex found in some bacteria and in all eukaryotic cells, and plays an important role in cellular physiology. Proteasomes are associated with the ubiquitin conjugation system (UCS), a major pathway for the degradation of cellular proteins of all types, including proteins that function to activate or repress cellular processes such as transcription and cell cycle progression (Ciechanover, A. (1994) *Cell* 79:13-21). In the UCS pathway, proteins targeted for degradation are conjugated to ubiquitin, a small heat stable protein. The ubiquitinated protein is then recognized and degraded by the proteasome. The resultant ubiquitin-peptide complex is hydrolyzed by a ubiquitin carboxyl terminal hydrolase, and free ubiquitin is released for reutilization by the UCS. Ubiquitin-proteasome systems are implicated in the degradation of mitotic cyclic kinases, oncoproteins, tumor suppressor genes (p53), cell surface receptors associated with signal transduction, transcriptional regulators, and mutated or damaged proteins (Ciechanover, *supra*). This pathway has been implicated in a number of diseases, including cystic fibrosis, Angelman's syndrome, and Liddle syndrome (reviewed in Schwartz, A.L. and A. Ciechanover (1999) *Annu. Rev. Med.* 50:57-74). A murine proto-oncogene, *Unp*, encodes a nuclear ubiquitin protease whose overexpression leads to oncogenic transformation of NIH3T3 cells. The human homologue of this gene is consistently elevated in small cell tumors and adenocarcinomas of the lung (Gray, D.A. (1995) *Oncogene* 10:2179-2183). Ubiquitin carboxyl terminal hydrolase is involved in the differentiation of a lymphoblastic leukemia cell line to a non-dividing mature state (Maki, A. et al. (1996) *Differentiation* 60:59-66). In neurons, ubiquitin carboxyl terminal hydrolase (PGP 9.5) expression is strong in the abnormal structures that occur in human neurodegenerative diseases (Lowe, J. et al. (1990) *J. Pathol.* 161:153-160). The proteasome is a large (~2000 kDa) multisubunit complex composed of a central catalytic core containing a variety of proteases arranged in four seven-membered rings with the active sites facing inwards into the central cavity, and terminal ATPase subunits covering the outer port of the cavity and regulating substrate entry (for review, see Schmidt, M. et al. (1999) *Curr. Opin. Chem. Biol.* 3:584-591).

Cysteine Proteases

Cysteine proteases (CPs) are involved in diverse cellular processes ranging from the processing of precursor proteins to intracellular degradation. Nearly half of the CPs known are present only in viruses. CPs have a cysteine as the major catalytic residue at the active site where catalysis proceeds via a thioester intermediate and is facilitated by nearby histidine and asparagine residues. A glutamine residue is also important, as it helps to form an oxyanion hole. Two important CP families include the

papain-like enzymes (C1) and the calpains (C2). Papain-like family members are generally lysosomal or secreted and therefore are synthesized with signal peptides as well as propeptides. Most members bear a conserved motif in the propeptide that may have structural significance (Karrer, K.M. et al. (1993) Proc. Natl. Acad. Sci. USA 90:3063-3067). Three-dimensional structures of papain family members show a bilobed molecule with the catalytic site located between the two lobes. Papains include cathepsins B, C, H, L, and S, certain plant allergens and dipeptidyl peptidase (for a review, see Rawlings, N.D. and A.J. Barrett (1994) Methods Enzymol. 244:461-486).

Some CPs are expressed ubiquitously, while others are produced only by cells of the immune system. Of particular note, CPs are produced by monocytes, macrophages and other cells which migrate to sites of inflammation and secrete molecules involved in tissue repair. Overabundance of these repair molecules plays a role in certain disorders. In autoimmune diseases such as rheumatoid arthritis, secretion of the cysteine peptidase cathepsin C degrades collagen, laminin, elastin and other structural proteins found in the extracellular matrix of bones. Bone weakened by such degradation is also more susceptible to tumor invasion and metastasis. Cathepsin L expression may also contribute to the influx of mononuclear cells which exacerbates the destruction of the rheumatoid synovium (Keyszer, G.M. (1995) Arthritis Rheum. 38:976-984).

Calpains are calcium-dependent cytosolic endopeptidases which contain both an N-terminal catalytic domain and a C-terminal calcium-binding domain. Calpain is expressed as a proenzyme heterodimer consisting of a catalytic subunit unique to each isoform and a regulatory subunit common to different isoforms. Each subunit bears a calcium-binding EF-hand domain. The regulatory subunit also contains a hydrophobic glycine-rich domain that allows the enzyme to associate with cell membranes. Calpains are activated by increased intracellular calcium concentration, which induces a change in conformation and limited autolysis. The resultant active molecule requires a lower calcium concentration for its activity (Chan, S.L. and M.P. Mattson (1999) J. Neurosci. Res. 58:167-190). Calpain expression is predominantly neuronal, although it is present in other tissues. Several chronic neurodegenerative disorders, including ALS, Parkinson's disease and Alzheimer's disease are associated with increased calpain expression (Chan and Mattson, *supra*). Calpain-mediated breakdown of the cytoskeleton has been proposed to contribute to brain damage resulting from head injury (McCracken, E. et al. (1999) J. Neurotrauma 16:749-761). Calpain-3 is predominantly expressed in skeletal muscle, and is responsible for limb-girdle muscular dystrophy type 2A (Minami, N. et al. (1999) J. Neurol. Sci. 171:31-37).

Another family of thiol proteases is the caspases, which are involved in the initiation and execution phases of apoptosis. A pro-apoptotic signal can activate initiator caspases that trigger a proteolytic caspase cascade, leading to the hydrolysis of target proteins and the classic apoptotic death

of the cell. Two active site residues, a cysteine and a histidine, have been implicated in the catalytic mechanism. Caspases are among the most specific endopeptidases, cleaving after aspartate residues. Caspases are synthesized as inactive zymogens consisting of one large (p20) and one small (p10) subunit separated by a small spacer region, and a variable N-terminal prodomain. This prodomain
5 interacts with cofactors that can positively or negatively affect apoptosis. An activating signal causes autoproteolytic cleavage of a specific aspartate residue (D297 in the caspase-1 numbering convention) and removal of the spacer and prodomain, leaving a p10/p20 heterodimer. Two of these heterodimers interact via their small subunits to form the catalytically active tetramer. The long prodomains of some caspase family members have been shown to promote dimerization and auto-processing of procaspases.
10 Some caspases contain a "death effector domain" in their prodomain by which they can be recruited into self-activating complexes with other caspases and FADD protein associated death receptors or the TNF receptor complex. In addition, two dimers from different caspase family members can associate, changing the substrate specificity of the resultant tetramer. Endogenous caspase inhibitors (inhibitor of apoptosis proteins, or IAPs) also exist. All these interactions have clear effects on the control of
15 apoptosis (reviewed in Chan and Mattson, supra; Salveson, G.S. and V.M. Dixit (1999) Proc. Natl. Acad. Sci. USA 96:10964-10967).

Caspases have been implicated in a number of diseases. Mice lacking some caspases have severe nervous system defects due to failed apoptosis in the neuroepithelium and suffer early lethality. Others show severe defects in the inflammatory response, as caspases are responsible for processing IL-
20 1b and possibly other inflammatory cytokines (Chan and Mattson, supra). Cowpox virus and baculoviruses target caspases to avoid the death of their host cell and promote successful infection. In addition, increases in inappropriate apoptosis have been reported in AIDS, neurodegenerative diseases and ischemic injury, while a decrease in cell death is associated with cancer (Salveson and Dixit, supra; Thompson, C.B. (1995) Science 267:1456-1462).

25 Aspartyl proteases

Aspartyl proteases (APs) include the lysosomal proteases cathepsins D and E, as well as chymosin, renin, and the gastric pepsins. Most retroviruses encode an AP, usually as part of the pol
polyprotein. APs, also called acid proteases, are monomeric enzymes consisting of two domains, each domain containing one half of the active site with its own catalytic aspartic acid residue. APs are most
30 active in the range of pH 2-3, at which one of the aspartate residues is ionized and the other neutral. The pepsin family of APs contains many secreted enzymes, and all are likely to be synthesized with signal peptides and propeptides. Most family members have three disulfide loops, the first ~5 residue loop following the first aspartate, the second 5-6 residue loop preceding the second aspartate, and the third and largest loop occurring toward the C terminus. Retropepsins, on the other hand, are analogous

to a single domain of pepsin, and become active as homodimers with each retropepsin monomer contributing one half of the active site. Retropepsins are required for processing the viral polyproteins.

APs have roles in various tissues, and some have been associated with disease. Renin mediates the first step in processing the hormone angiotensin, which is responsible for regulating electrolyte balance and blood pressure (reviewed in Crews, D.E. and S.R. Williams (1999) *Hum. Biol.* 71:475-503). Abnormal regulation and expression of cathepsins are evident in various inflammatory disease states. Expression of cathepsin D is elevated in synovial tissues from patients with rheumatoid arthritis and osteoarthritis. The increased expression and differential regulation of the cathepsins are linked to the metastatic potential of a variety of cancers (Chambers, A.F. et al. (1993) *Crit. Rev. Oncol.* 4:95-114).

Metalloproteases

Metalloproteases require a metal ion for activity, usually manganese or zinc. Examples of manganese metalloenzymes include aminopeptidase P and human proline dipeptidase (PEPD). Aminopeptidase P can degrade bradykinin, a nonapeptide activated in a variety of inflammatory responses. Aminopeptidase P has been implicated in coronary ischemia/reperfusion injury. Administration of aminopeptidase P inhibitors has been shown to have a cardioprotective effect in rats (Ersahin, C. et al (1999) *J. Cardiovasc. Pharmacol.* 34:604-611).

Most zinc-dependent metalloproteases share a common sequence in the zinc-binding domain. The active site is made up of two histidines which act as zinc ligands and a catalytic glutamic acid C-terminal to the first histidine. Proteins containing this signature sequence are known as the metzincins and include aminopeptidases B and N, angiotensin-converting enzyme, neurolysin, the matrix metalloproteases and the adamalysins (ADAMS). An alternate sequence is found in the zinc carboxypeptidases, in which all three conserved residues – two histidines and a glutamic acid – are involved in zinc binding.

A number of the neutral metalloendopeptidases, including angiotensin converting enzyme and the aminopeptidases, are involved in the metabolism of peptide hormones. High aminopeptidase B activity, for example, is found in the adrenal glands and neurohypophyses of hypertensive rats (Prieto, I. et al. (1998) *Horm. Metab. Res.* 30:246-248). Oligopeptidase M/neurolysin can hydrolyze bradykinin as well as neurotensin (Serizawa, A. et al. (1995) *J. Biol. Chem.* 270:2092-2098). Neurotensin is a vasoactive peptide that can act as a neurotransmitter in the brain, where it has been implicated in limiting food intake (Tritos, N.A. et al. (1999) *Neuropeptides* 33:339-349).

The matrix metalloproteases (MMPs) are a family of at least 23 enzymes that can degrade components of the extracellular matrix (ECM). They are Zn^{+2} endopeptidases with an N-terminal catalytic domain. Nearly all members of the family have a hinge peptide and C-terminal domain which

can bind to substrate molecules in the ECM or to inhibitors produced by the tissue (TIMPs, for tissue inhibitor of metalloprotease; Campbell, I.L. et al. (1999) Trends Neurosci. 22:285). The presence of fibronectin-like repeats, transmembrane domains, or C-terminal hemopexinase-like domains can be used to separate MMPs into collagenase, gelatinase, stromelysin and membrane-type MMP subfamilies. In the inactive form, the Zn^{+2} ion in the active site interacts with a cysteine in the pro-sequence. Activating factors disrupt the Zn^{+2} -cysteine interaction, or "cysteine switch," exposing the active site. This partially activates the enzyme, which then cleaves off its propeptide and becomes fully active. MMPs are often activated by the serine proteases plasmin and furin. MMPs are often regulated by stoichiometric, noncovalent interactions with inhibitors; the balance of protease to inhibitor, then, is very important in tissue homeostasis (reviewed in Yong, V.W. et al. (1998) Trends Neurosci. 21:75). Ehlers-Danlos syndrome type VII C is caused by mutations in the procollagen I N-proteinase gene (Colige, A. et al. (1999) Am. J. Hum. Genet. 65:308-317).

MMPs are implicated in a number of diseases including osteoarthritis (Mitchell, P. et al. (1996) J. Clin. Invest. 97:761), atherosclerotic plaque rupture (Sukhova, G.K. et al. (1999) Circulation 99:2503), aortic aneurysm (Schneiderman, J. et al. (1998) Am. J. Path. 152:703), non-healing wounds (Saarialho-Kere, U.K. et al. (1994) J. Clin. Invest. 94:79), bone resorption (Blavier, L. and J.M. Delaisse (1995) J. Cell Sci. 108:3649), age-related macular degeneration (Steen, B. et al. (1998) Invest. Ophthalmol. Vis. Sci. 39:2194), emphysema (Finlay, G.A. et al. (1997) Thorax 52:502), myocardial infarction (Rohde, L.E. et al. (1999) Circulation 99:3063) and dilated cardiomyopathy (Thomas, C.V. et al. (1998) Circulation 97:1708). MMP inhibitors prevent metastasis of mammary carcinoma and experimental tumors in rat, and Lewis lung carcinoma, hemangioma, and human ovarian carcinoma xenografts in mice (Eccles, S.A. et al. (1996) Cancer Res. 56:2815; Anderson et al. (1996) Cancer Res. 56:715-718; Volpert, O.V. et al. (1996) J. Clin. Invest. 98:671; Taraboletti, G. et al. (1995) J. NCI 87:293; Davies, B. et al. (1993) Cancer Res. 53:2087). MMPs may be active in Alzheimer's disease. A number of MMPs are implicated in multiple sclerosis, and administration of MMP inhibitors can relieve some of its symptoms (reviewed in Yong, *supra*).

Another family of metalloproteases is the ADAMs, for A Disintegrin and Metalloprotease Domain, which they share with their close relatives the adamalysins, snake venom metalloproteases (SVMPs). ADAMs combine features of both cell surface adhesion molecules and proteases, containing a prodomain, a protease domain, a disintegrin domain, a cysteine rich domain, an epidermal growth factor repeat, a transmembrane domain, and a cytoplasmic tail. The first three domains listed above are also found in the SVMPs. The ADAMs possess four potential functions: proteolysis, adhesion, signaling and fusion. The ADAMs share the metzincin zinc binding sequence and are inhibited by some MMP antagonists such as TIMP-1.

ADAMs are implicated in such processes as sperm-egg binding and fusion, myoblast fusion, and protein-ectodomain processing or shedding of cytokines, cytokine receptors, adhesion proteins and other extracellular protein domains (Schlöndorff, J. and C.P. Blobel (1999) J. Cell. Sci. 112:3603-3617). The Kuzbanian protein cleaves a substrate in the NOTCH pathway (possibly NOTCH itself),
5 activating the program for lateral inhibition in Drosophila neural development. Two ADAMs, TACE (ADAM 17) and ADAM 10, are proposed to have analogous roles in the processing of amyloid precursor protein in the brain (Schlöndorff and Blobel, supra). TACE has also been identified as the TNF activating enzyme (Black, R.A. et al. (1997) Nature 385:729). TNF is a pleiotropic cytokine that is important in mobilizing host defenses in response to infection or trauma, but can cause severe
10 damage in excess and is often overproduced in autoimmune disease. TACE cleaves membrane-bound pro-TNF to release a soluble form. Other ADAMs may be involved in a similar type of processing of other membrane-bound molecules.

The ADAMTS sub-family has all of the features of ADAM family metalloproteases and contain an additional thrombospondin domain (TS). The prototypic ADAMTS was identified in mouse,
15 found to be expressed in heart and kidney and upregulated by proinflammatory stimuli (Kuno, K. et al. (1997) J. Biol. Chem. 272:556-562). To date eleven members are recognized by the Human Genome Organization (HUGO; <http://www.gene.ucl.ac.uk/users/hester/adamts.html#Approved>). Members of this family have the ability to degrade aggrecan, a high molecular weight proteoglycan which provides cartilage with important mechanical properties including compressibility, and which is lost during the
20 development of arthritis. Enzymes which degrade aggrecan are thus considered attractive targets to prevent and slow the degradation of articular cartilage (See, e.g., Tortorella, M.D. (1999) Science 284:1664; Abbaszade, I. (1999) J. Biol. Chem. 274:23443). Other members are reported to have antiangiogenic potential (Kuno et al., supra) and/or procollagen processing (Colige, A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:2374).

25 The discovery of new proteases and the polynucleotides encoding them satisfies a need in the art by providing new compositions which are useful in hydrolysis of peptide bonds and in the diagnosis, prevention, and treatment of gastrointestinal, cardiovascular, autoimmune/inflammatory, cell proliferative, developmental, epithelial, neurological, and reproductive disorders, and in the assessment of the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of
30 proteases.

SUMMARY OF THE INVENTION

The invention features purified polypeptides, proteases, referred to collectively as "PRTS" and individually as "PRTS-1," "PRTS-2," "PRTS-3," "PRTS-4," "PRTS-5," "PRTS-6," "PRTS-7,"

"PRTS-8," "PRTS-9," "PRTS-10," "PRTS-11," "PRTS-12," "PRTS-13," "PRTS-14," "PRTS-15," "PRTS-16," "PRTS-17," "PRTS-18," "PRTS-19," "PRTS-20," and "PRTS-21." In one aspect, the invention provides an isolated polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21. In one alternative, the invention provides an isolated polypeptide comprising the amino acid sequence of SEQ ID NO:1-21.

The invention further provides an isolated polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21. In one alternative, the polynucleotide encodes a polypeptide selected from the group consisting of SEQ ID NO:1-21. In another alternative, the polynucleotide is selected from the group consisting of SEQ ID NO:22-42.

Additionally, the invention provides a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21. In one alternative, the invention provides a cell transformed with the recombinant polynucleotide. In another alternative, the invention provides a transgenic organism comprising the recombinant polynucleotide.

The invention also provides a method for producing a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group

consisting of SEQ ID NO:1-21, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21. The method comprises a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide encoding the polypeptide, and b) recovering the polypeptide so expressed.

Additionally, the invention provides an isolated antibody which specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21.

The invention further provides an isolated polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:22-42, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:22-42, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). In one alternative, the polynucleotide comprises at least 60 contiguous nucleotides.

Additionally, the invention provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:22-42, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:22-42, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and b) detecting the presence or absence of said hybridization complex, and optionally, if present, the amount thereof. In one alternative, the probe comprises at least 60 contiguous nucleotides.

The invention further provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide selected from the group consisting of a) a

polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:22-42, b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:22-42, c) a polynucleotide complementary to the polynucleotide of a), d) a polynucleotide complementary to the polynucleotide of b), and e) an RNA equivalent of a)-d). The method comprises a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

The invention further provides a composition comprising an effective amount of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, and a pharmaceutically acceptable excipient. In one embodiment, the composition comprises an amino acid sequence selected from the group consisting of SEQ ID NO:1-21. The invention additionally provides a method of treating a disease or condition associated with decreased expression of functional PRTS, comprising administering to a patient in need of such treatment the composition.

The invention also provides a method for screening a compound for effectiveness as an agonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. In one alternative, the invention provides a composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with decreased expression of functional PRTS, comprising administering to a patient in need of such treatment the composition.

Additionally, the invention provides a method for screening a compound for effectiveness as an antagonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an

amino acid sequence selected from the group consisting of SEQ ID NO:1-21, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, and
5 d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample. In one alternative, the invention provides a composition comprising an antagonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of
10 treating a disease or condition associated with overexpression of functional PRTS, comprising administering to a patient in need of such treatment the composition.

The invention further provides a method of screening for a compound that specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, b) a polypeptide comprising a
15 naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21. The method comprises a) combining the polypeptide with at least one test compound under
20 suitable conditions, and b) detecting binding of the polypeptide to the test compound, thereby identifying a compound that specifically binds to the polypeptide.

The invention further provides a method of screening for a compound that modulates the activity of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, b) a polypeptide comprising a
25 naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21. The method comprises a) combining the polypeptide with at least one test compound under
30 conditions permissive for the activity of the polypeptide, b) assessing the activity of the polypeptide in the presence of the test compound, and c) comparing the activity of the polypeptide in the presence of the test compound with the activity of the polypeptide in the absence of the test compound, wherein a change in the activity of the polypeptide in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide.

The invention further provides a method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence selected from the group consisting of SEQ ID NO:22-42, the method comprising a) exposing a sample comprising the target polynucleotide to a compound, and b) detecting altered expression of the target polynucleotide.

The invention further provides a method for assessing toxicity of a test compound, said method comprising a) treating a biological sample containing nucleic acids with the test compound; b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:22-42, ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:22-42, iii) a polynucleotide having a sequence complementary to i), iv) a polynucleotide complementary to the polynucleotide of ii), and v) an RNA equivalent of i)-iv). Hybridization occurs under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:22-42, ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:22-42, iii) a polynucleotide complementary to the polynucleotide of i), iv) a polynucleotide complementary to the polynucleotide of ii), and v) an RNA equivalent of i)-iv). Alternatively, the target polynucleotide comprises a fragment of a polynucleotide sequence selected from the group consisting of i)-v) above; c) quantifying the amount of hybridization complex; and d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

BRIEF DESCRIPTION OF THE TABLES

Table 1 summarizes the nomenclature for the full length polynucleotide and polypeptide sequences of the present invention.

Table 2 shows the GenBank identification number and annotation of the nearest GenBank homolog for polypeptides of the invention. The probability score for the match between each polypeptide and its GenBank homolog is also shown.

Table 3 shows structural features of polypeptide sequences of the invention, including predicted motifs and domains, along with the methods, algorithms, and searchable databases used for analysis of the polypeptides.

5 Table 4 lists the cDNA and/or genomic DNA fragments which were used to assemble polynucleotide sequences of the invention, along with selected fragments of the polynucleotide sequences.

Table 5 shows the representative cDNA library for polynucleotides of the invention.

Table 6 provides an appendix which describes the tissues and vectors used for construction of the cDNA libraries shown in Table 5.

10 Table 7 shows the tools, programs, and algorithms used to analyze the polynucleotides and polypeptides of the invention, along with applicable descriptions, references, and threshold parameters.

DESCRIPTION OF THE INVENTION

Before the present proteins, nucleotide sequences, and methods are described, it is understood
15 that this invention is not limited to the particular machines, materials and methods described, as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an,"
20 and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a host cell" includes a plurality of such host cells, and a reference to "an antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meanings
25 as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any machines, materials, and methods similar or equivalent to those described herein can be used to practice or test the present invention, the preferred machines, materials and methods are now described. All publications mentioned herein are cited for the purpose of describing and disclosing the cell lines, protocols, reagents and vectors which are reported in the publications and which might be used in
30 connection with the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

"PRTS" refers to the amino acid sequences of substantially purified PRTS obtained from any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and human, and from any source, whether natural, synthetic, semi-synthetic, or recombinant.

The term "agonist" refers to a molecule which intensifies or mimics the biological activity of PRTS. Agonists may include proteins, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of PRTS either by directly interacting with PRTS or by acting on components of the biological pathway in which PRTS participates.

An "allelic variant" is an alternative form of the gene encoding PRTS. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. A gene may have none, one, or many allelic variants of its naturally occurring form. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

"Altered" nucleic acid sequences encoding PRTS include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as PRTS or a polypeptide with at least one functional characteristic of PRTS. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding PRTS, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding PRTS. The encoded protein may also be "altered," and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent PRTS. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of PRTS is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, and positively charged amino acids may include lysine and arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine. Amino acids with uncharged side chains having similar hydrophobicity values may include: leucine, isoleucine, and valine; glycine and alanine; and phenylalanine and tyrosine.

The terms "amino acid" and "amino acid sequence" refer to an oligopeptide, peptide, polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring or synthetic

molecules. Where "amino acid sequence" is recited to refer to a sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

"Amplification" relates to the production of additional copies of a nucleic acid sequence.

- 5 Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art.

The term "antagonist" refers to a molecule which inhibits or attenuates the biological activity of PRTS. Antagonists may include proteins such as antibodies, nucleic acids, carbohydrates, small molecules, or any other compound or composition which modulates the activity of PRTS either by
10 directly interacting with PRTS or by acting on components of the biological pathway in which PRTS participates.

The term "antibody" refers to intact immunoglobulin molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding an epitopic determinant. Antibodies that bind PRTS polypeptides can be prepared using intact polypeptides or using fragments
15 containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

20 The term "antigenic determinant" refers to that region of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (particular regions or three-dimensional structures on the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to
25 elicit the immune response) for binding to an antibody.

The term "antisense" refers to any composition capable of base-pairing with the "sense" (coding) strand of a specific nucleic acid sequence. Antisense compositions may include DNA; RNA; peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as
30 phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine. Antisense molecules may be produced by any method including chemical synthesis or transcription. Once introduced into a cell, the complementary antisense molecule base-pairs with a naturally occurring nucleic acid sequence produced by the cell to form duplexes which block either transcription or

translation. The designation "negative" or "minus" can refer to the antisense strand, and the designation "positive" or "plus" can refer to the sense strand of a reference DNA molecule.

The term "biologically active" refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" or "immunogenic" refers to the capability of the natural, recombinant, or synthetic PRTS, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

"Complementary" describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing. For example, 5'-AGT-3' pairs with its complement, 3'-TCA-5'.

A "composition comprising a given polynucleotide sequence" and a "composition comprising a given amino acid sequence" refer broadly to any composition containing the given polynucleotide or amino acid sequence. The composition may comprise a dry formulation or an aqueous solution. Compositions comprising polynucleotide sequences encoding PRTS or fragments of PRTS may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilizing agent such as a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts (e.g., NaCl), detergents (e.g., sodium dodecyl sulfate; SDS), and other components (e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

"Consensus sequence" refers to a nucleic acid sequence which has been subjected to repeated DNA sequence analysis to resolve uncalled bases, extended using the XL-PCR kit (Applied Biosystems, Foster City CA) in the 5' and/or the 3' direction, and resequenced, or which has been assembled from one or more overlapping cDNA, EST, or genomic DNA fragments using a computer program for fragment assembly, such as the GELVIEW fragment assembly system (GCG, Madison WI) or Phrap (University of Washington, Seattle WA). Some sequences have been both extended and assembled to produce the consensus sequence.

"Conservative amino acid substitutions" are those substitutions that are predicted to least interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is conserved and not significantly changed by such substitutions. The table below shows amino acids which may be substituted for an original amino acid in a protein and which are regarded as conservative amino acid substitutions.

Original Residue	Conservative Substitution
Ala	Gly, Ser
Arg	His, Lys
Asn	Asp, Gln, His
Asp	Asn, Glu

	Cys	Ala, Ser
	Gln	Asn, Glu, His
	Glu	Asp, Gln, His
	Gly	Ala
5	His	Asn, Arg, Gln, Glu
	Ile	Leu, Val
	Leu	Ile, Val
	Lys	Arg, Gln, Glu
	Met	Leu, Ile
10	Phe	His, Met, Leu, Trp, Tyr
	Ser	Cys, Thr
	Thr	Ser, Val
	Trp	Phe, Tyr
	Tyr	His, Phe, Trp
15	Val	Ile, Leu, Thr

Conservative amino acid substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the site of the substitution, and/or (c) the bulk of the side chain.

A "deletion" refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

The term "derivative" refers to a chemically modified polynucleotide or polypeptide. Chemical modifications of a polynucleotide can include, for example, replacement of hydrogen by an alkyl, acyl, hydroxyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one biological or immunological function of the natural molecule. A derivative polypeptide is one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

A "detectable label" refers to a reporter molecule or enzyme that is capable of generating a measurable signal and is covalently or noncovalently joined to a polynucleotide or polypeptide.

"Differential expression" refers to increased or upregulated; or decreased, downregulated, or absent gene or protein expression, determined by comparing at least two different samples. Such comparisons may be carried out between, for example, a treated and an untreated sample, or a diseased and a normal sample.

A "fragment" is a unique portion of PRTS or the polynucleotide encoding PRTS which is identical in sequence to but shorter in length than the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from 5 to 1000 contiguous nucleotides or amino acid residues. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10,

15, 16, 20, 25, 30, 40, 50, 60, 75, 100, 150, 250 or at least 500 contiguous nucleotides or amino acid residues in length. Fragments may be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50%) of a polypeptide as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, including the Sequence Listing, tables, and figures, may be encompassed by the present embodiments.

A fragment of SEQ ID NO:22-42 comprises a region of unique polynucleotide sequence that specifically identifies SEQ ID NO:22-42, for example, as distinct from any other sequence in the genome from which the fragment was obtained. A fragment of SEQ ID NO:22-42 is useful, for example, in hybridization and amplification technologies and in analogous methods that distinguish SEQ ID NO:22-42 from related polynucleotide sequences. The precise length of a fragment of SEQ ID NO:22-42 and the region of SEQ ID NO:22-42 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A fragment of SEQ ID NO:1-21 is encoded by a fragment of SEQ ID NO:22-42. A fragment of SEQ ID NO:1-21 comprises a region of unique amino acid sequence that specifically identifies SEQ ID NO:1-21. For example, a fragment of SEQ ID NO:1-21 is useful as an immunogenic peptide for the development of antibodies that specifically recognize SEQ ID NO:1-21. The precise length of a fragment of SEQ ID NO:1-21 and the region of SEQ ID NO:1-21 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A "full length" polynucleotide sequence is one containing at least a translation initiation codon (e.g., methionine) followed by an open reading frame and a translation termination codon. A "full length" polynucleotide sequence encodes a "full length" polypeptide sequence.

"Homology" refers to sequence similarity or, interchangeably, sequence identity, between two or more polynucleotide sequences or two or more polypeptide sequences.

The terms "percent identity" and "% identity," as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences.

Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL Y algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular

biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and P.M. Sharp (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS 8:189-191.

For pairwise alignments of polynucleotide sequences, the default parameters are set as follows:

5 Ktuple=2, gap penalty=5, window=4, and "diagonals saved"=4. The "weighted" residue weight table is selected as the default. Percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polynucleotide sequences.

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several
10 sources, including the NCBI, Bethesda, MD, and on the Internet at <http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence analysis programs including "blastn," that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2
15 Sequences" can be accessed and used interactively at <http://www.ncbi.nlm.nih.gov/gorf/bl2.html>. The "BLAST 2 Sequences" tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the "BLAST 2 Sequences" tool Version 2.0.12 (April-21-2000) set at default parameters. Such default parameters may be, for example:

20 *Matrix: BLOSUM62*
Reward for match: 1
Penalty for mismatch: -2
Open Gap: 5 and Extension Gap: 2 penalties
Gap x drop-off: 50
25 *Expect: 10*
Word Size: 11
Filter: on

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over
30 the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures, or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in a nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

5 The phrases "percent identity" and "% identity," as applied to polypeptide sequences, refer to the percentage of residue matches between at least two polypeptide sequences aligned using a standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the charge and hydrophobicity at the site of
10 substitution, thus preserving the structure (and therefore function) of the polypeptide.

Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and
15 "diagonals saved"=5. The PAM250 matrix is selected as the default residue weight table. As with polynucleotide alignments, the percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polypeptide sequence pairs.

Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the "BLAST 2 Sequences" tool Version 2.0.12
20 (April-21-2000) with blastp set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Open Gap: 11 and Extension Gap: 1 penalties

Gap x drop-off: 50

Expect: 10

25 *Word Size: 3*

Filter: on

Percent identity may be measured over the length of an entire defined polypeptide sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance,
30 a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in the tables, figures or Sequence Listing, may be used to describe a length over which percentage identity may be measured.

"Human artificial chromosomes" (HACs) are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size and which contain all of the elements required for chromosome replication, segregation and maintenance.

The term "humanized antibody" refers to an antibody molecule in which the amino acid sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

"Hybridization" refers to the process by which a polynucleotide strand anneals with a complementary strand through base pairing under defined hybridization conditions. Specific hybridization is an indication that two nucleic acid sequences share a high degree of complementarity. Specific hybridization complexes form under permissive annealing conditions and remain hybridized after the "washing" step(s). The washing step(s) is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid strands that are not perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable by one of ordinary skill in the art and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency, and therefore hybridization specificity. Permissive annealing conditions occur, for example, at 68°C in the presence of about 6 x SSC, about 1% (w/v) SDS, and about 100 µg/ml sheared, denatured salmon sperm DNA.

Generally, stringency of hybridization is expressed, in part, with reference to the temperature under which the wash step is carried out. Such wash temperatures are typically selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating T_m and conditions for nucleic acid hybridization are well known and can be found in Sambrook, J. et al. (1989) Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour. Alternatively, temperatures of about 65°C, 60°C, 55°C, or 42°C may be used. SSC concentration may be varied from about 0.1 to 2 x SSC, with SDS being present at about 0.1%. Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, sheared and denatured salmon sperm DNA at about 100-200 µg/ml. Organic solvent, such as formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as for RNA:DNA hybridizations. Useful variations on these wash conditions will be readily

apparent to those of ordinary skill in the art. Hybridization, particularly under high stringency conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their encoded polypeptides.

5 The term "hybridization complex" refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., C₀t or R₀t analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed).

10 The words "insertion" and "addition" refer to changes in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively.

"Immune response" can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular
15 and systemic defense systems.

An "immunogenic fragment" is a polypeptide or oligopeptide fragment of PRTS which is capable of eliciting an immune response when introduced into a living organism, for example, a mammal. The term "immunogenic fragment" also includes any polypeptide or oligopeptide fragment of PRTS which is useful in any of the antibody production methods disclosed herein or known in the art.

20 The term "microarray" refers to an arrangement of a plurality of polynucleotides, polypeptides, or other chemical compounds on a substrate.

The terms "element" and "array element" refer to a polynucleotide, polypeptide, or other chemical compound having a unique and defined position on a microarray.

25 The term "modulate" refers to a change in the activity of PRTS. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of PRTS.

The phrases "nucleic acid" and "nucleic acid sequence" refer to a nucleotide, oligonucleotide, polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the
30 antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material.

"Operably linked" refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with a second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding

sequence. Operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

“Peptide nucleic acid” (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell.

“Post-translational modification” of an PRTS may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the art. These processes may occur synthetically or biochemically. Biochemical modifications will vary by cell type depending on the enzymatic milieu of PRTS.

“Probe” refers to nucleic acid sequences encoding PRTS, their complements, or fragments thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule. Typical labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes. “Primers” are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing. The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

Probes and primers as used in the present invention typically comprise at least 15 contiguous nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the specification, including the tables, figures, and Sequence Listing, may be used.

Methods for preparing and using probes and primers are described in the references, for example Sambrook, J. et al. (1989) Molecular Cloning: A Laboratory Manual, 2nd ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; Ausubel, F.M. et al. (1987) Current Protocols in Molecular Biology, Greene Publ. Assoc. & Wiley-Intersciences, New York NY; Innis, M. et al. (1990) PCR Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA. PCR primer pairs can be derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection

5 programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3 primer selection

10 program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user's specific needs.) The PrimeGen program

15 (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing

20 primers, microarray elements, or specific probes to identify fully or partially complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

A "recombinant nucleic acid" is a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two or more otherwise separated segments of sequence.

25 This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques such as those described in Sambrook, *supra*. The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence.

30 Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a vaccinia virus, that could be use to vaccinate a mammal wherein the recombinant nucleic acid is expressed, inducing a protective immunological response in the mammal.

A "regulatory element" refers to a nucleic acid sequence usually derived from untranslated regions of a gene and includes enhancers, promoters, introns, and 5' and 3' untranslated regions (UTRs). Regulatory elements interact with host or viral proteins which control transcription, translation, or RNA stability.

5 "Reporter molecules" are chemical or biochemical moieties used for labeling a nucleic acid, amino acid, or antibody. Reporter molecules include radionuclides; enzymes; fluorescent, chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and other moieties known in the art.

An "RNA equivalent," in reference to a DNA sequence, is composed of the same linear
10 sequence of nucleotides as the reference DNA sequence with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The term "sample" is used in its broadest sense. A sample suspected of containing PRTS, nucleic acids encoding PRTS, or fragments thereof may comprise a bodily fluid; an extract from a cell,
15 chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

The terms "specific binding" and "specifically binding" refer to that interaction between a protein or peptide and an agonist, an antibody, an antagonist, a small molecule, or any natural or synthetic binding composition. The interaction is dependent upon the presence of a particular structure
20 of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide comprising the epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

The term "substantially purified" refers to nucleic acid or amino acid sequences that are
25 removed from their natural environment and are isolated or separated, and are at least 60% free, preferably at least 75% free, and most preferably at least 90% free from other components with which they are naturally associated.

A "substitution" refers to the replacement of one or more amino acid residues or nucleotides by different amino acid residues or nucleotides, respectively.

30 "Substrate" refers to any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

A "transcript image" refers to the collective pattern of gene expression by a particular cell type or tissue under given conditions at a given time.

"Transformation" describes a process by which exogenous DNA is introduced into a recipient cell. Transformation may occur under natural or artificial conditions according to various methods well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based on the type of host cell being transformed and may include, but is not limited to, bacteriophage or viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term "transformed cells" includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for limited periods of time.

A "transgenic organism," as used herein, is any organism, including but not limited to animals and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or in vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, plants and animals. The isolated DNA of the present invention can be introduced into the host by methods known in the art, for example infection, transfection, transformation or transconjugation. Techniques for transferring the DNA of the present invention into such organisms are widely known and provided in references such as Sambrook et al. (1989), supra.

A "variant" of a particular nucleic acid sequence is defined as a nucleic acid sequence having at least 40% sequence identity to the particular nucleic acid sequence over a certain length of one of the nucleic acid sequences using blastn with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of nucleic acids may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length. A variant may be described as, for example, an "allelic" (as defined above), "splice," "species," or "polymorphic" variant. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternative splicing of exons during mRNA processing. The corresponding polypeptide may

possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides will generally have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one nucleotide base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at least 40% sequence identity to the particular polypeptide sequence over a certain length of one of the polypeptide sequences using blastp with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length of one of the polypeptides.

THE INVENTION

The invention is based on the discovery of new human proteases (PRTS), the polynucleotides encoding PRTS, and the use of these compositions for the diagnosis, treatment, or prevention of gastrointestinal, cardiovascular, autoimmune/inflammatory, cell proliferative, developmental, epithelial, neurological, and reproductive disorders.

Table 1 summarizes the nomenclature for the full length polynucleotide and polypeptide sequences of the invention. Each polynucleotide and its corresponding polypeptide are correlated to a single Incyte project identification number (Incyte Project ID). Each polypeptide sequence is denoted by both a polypeptide sequence identification number (Polypeptide SEQ ID NO:) and an Incyte polypeptide sequence number (Incyte Polypeptide ID) as shown. Each polynucleotide sequence is denoted by both a polynucleotide sequence identification number (Polynucleotide SEQ ID NO:) and an Incyte polynucleotide consensus sequence number (Incyte Polynucleotide ID) as shown.

Table 2 shows sequences with homology to the polypeptides of the invention as identified by BLAST analysis against the GenBank protein (genpept) database. Columns 1 and 2 show the polypeptide sequence identification number (Polypeptide SEQ ID NO:) and the corresponding Incyte polypeptide sequence number (Incyte Polypeptide ID) for polypeptides of the invention. Column 3 shows the GenBank identification number (Genbank ID NO:) of the nearest GenBank homolog. Column 4 shows the probability score for the match between each polypeptide and its GenBank

homolog. Column 5 shows the annotation of the GenBank homolog along with relevant citations where applicable, all of which are expressly incorporated by reference herein.

Table 3 shows various structural features of the polypeptides of the invention. Columns 1 and 2 show the polypeptide sequence identification number (SEQ ID NO:) and the corresponding Incyte polypeptide sequence number (Incyte Polypeptide ID) for each polypeptide of the invention. Column 3 shows the number of amino acid residues in each polypeptide. Column 4 shows potential phosphorylation sites, and column 5 shows potential glycosylation sites, as determined by the MOTIFS program of the GCG sequence analysis software package (Genetics Computer Group, Madison WI). Column 6 shows amino acid residues comprising signature sequences, domains, and motifs. Column 7 shows analytical methods for protein structure/function analysis and in some cases, searchable databases to which the analytical methods were applied.

Together, Tables 2 and 3 summarize the properties of polypeptides of the invention, and these properties establish that the claimed polypeptides are proteases. For example, SEQ ID NO:1 is a ubiquitin carboxyl terminal hydrolase. SEQ ID NO:1 is 48% identical, from residue M1 to residue G225, to human ubiquitin-specific processing protease (GenBank ID g9971757) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $1.00e-49$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:1 contains a ubiquitin carboxyl terminal hydrolase catalytic site domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. The score is 53.4 bits and the E-value is $4.9e-12$, which indicates the probability of obtaining the observed structural motif by chance. The presence of this motif was corroborated by BLIMPS (probability score= $2.6e-4$) and MOTIFS analyses. This provides further evidence that SEQ ID NO:1 is a ubiquitin carboxyl-terminal hydrolase. In an alternative example, SEQ ID NO:2 is 45% identical to amino acids 15-235 of human prostatic, a serine protease (GenBank ID g1143194) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $1.3e-46$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:2 also contains a trypsin family serine protease active site domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. This match has a probability score of $2.7e-58$. BLIMPS, MOTIFS, and PROFILESCAN analyses confirm the presence of this domain. (See Table 3.) BLIMPS analysis also reveals a kringle domain, providing further corroborative evidence that SEQ ID NO:2 is a serine protease of the trypsin family. In an alternative example, SEQ ID NO:7 is a dipeptidase which hydrolyses a variety of peptides (Kozak, E. and S. Tate (1982) J. Biol. Chem. 257:6322-6327), and is responsible for the hydrolysis of the beta

lactam rings of antibiotics such as penem and carbapenem (Campbell et al., (1984) J. Biol. Chem. 259:14586-14590). SEQ ID NO:7 shows 48% amino acid sequence identity over 377 amino acids (total length equals 411 amino acids) to human dipeptidase precursor (GenBank ID g219600) as determined by Basic Local Alignment Search Tool (BLAST). The BLAST probability score is $1.1e-88$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. Additionally, the protease of the invention demonstrates a renal dipeptidase domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. The HMM score for the renal dipeptidase PFAM hit is 412.7. Data from BLIMPS, MOTIFS, BLAST-DOMO, and BLAST-PRODOM analyses provide further corroborative evidence that SEQ ID NO:7 is a renal dipeptidase. The BLIMPS-BLOCKS hit scores for localized regions range from 1040-1537. The BLAST-DOMO hit probability score is $5.2e-85$. The BLAST-PRODOM hit probability score is $4.7e-73$. In an alternative example, SEQ ID NO:8 is 86% identical to human transmembrane trypsin (GenBank ID g6103629) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $3.9e-166$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:8 contains a trypsin family protease active site domain with a probability score of $5.3e-89$ as determined by searching for matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. BLIMPS, MOTIFS, and PROFILESCAN analyses confirm the presence of this motif. BLIMPS analysis also shows that SEQ ID NO:8 contains a kringle domain and a type I fibronectin domain. HMMER-based analysis reveals the presence of a transmembrane domain (See Table 3.). Taken together, these analyses show that SEQ ID NO:8 is a transmembrane member of the trypsin family of serine proteases. In an alternative example, SEQ ID NO:17 shares 44% local identity with human membrane-type serine protease 1 (MT-SP1, GenBank ID g6002714) as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is $5.1e-94$, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO:17 contains a trypsin family serine protease active site domain as determined by searching for statistically significant matches in the hidden Markov model (HMM)-based PFAM database of conserved protein family domains. (See Table 3.) HMM-based analysis also reveals a transmembrane domain near the N-terminus of SEQ ID NO:17. A domain found in the low-density lipoprotein receptor and other proteins, including MT-SP1 (PDOC00929) was also identified in this way. The presence of the trypsin active site motif is confirmed by PROFILESCAN, BLIMPS, and MOTIFS analyses. BLIMPS analysis revealed the presence of kringle and type I fibronectin domains. Taken together, these data provide further corroborative evidence that SEQ ID NO:17 is a transmembrane member of the trypsin family of serine proteases. SEQ ID NO:3-6, SEQ ID NO:9-16,

and SEQ ID NO:18-21 were analyzed and annotated in a similar manner. The algorithms and parameters for the analysis of SEQ ID NO:1-21 are described in Table 7.

As shown in Table 4, the full length polynucleotide sequences of the present invention were assembled using cDNA sequences or coding (exon) sequences derived from genomic DNA, or any combination of these two types of sequences. Columns 1 and 2 list the polynucleotide sequence identification number (Polynucleotide SEQ ID NO:) and the corresponding Incyte polynucleotide consensus sequence number (Incyte Polynucleotide ID) for each polynucleotide of the invention. Column 3 shows the length of each polynucleotide sequence in basepairs. Column 4 lists fragments of the polynucleotide sequences which are useful, for example, in hybridization or amplification technologies that identify SEQ ID NO:22-42 or that distinguish between SEQ ID NO:22-42 and related polynucleotide sequences. Column 5 shows identification numbers corresponding to cDNA sequences, coding sequences (exons) predicted from genomic DNA, and/or sequence assemblages comprised of both cDNA and genomic DNA. These sequences were used to assemble the full length polynucleotide sequences of the invention. Columns 6 and 7 of Table 4 show the nucleotide start (5') and stop (3') positions of the cDNA and/or genomic sequences in column 5 relative to their respective full length sequences.

The identification numbers in Column 5 of Table 4 may refer specifically, for example, to Incyte cDNAs along with their corresponding cDNA libraries. For example, 7246467T8 is the identification number of an Incyte cDNA sequence, and PROSTMY01 is the cDNA library from which it is derived. Incyte cDNAs for which cDNA libraries are not indicated were derived from pooled cDNA libraries (e.g., 71041539V1). Alternatively, the identification numbers in column 5 may refer to GenBank cDNAs or ESTs (e.g., g5745066) which contributed to the assembly of the full length polynucleotide sequences. Alternatively, the identification numbers in column 5 may refer to coding regions predicted by Genscan analysis of genomic DNA. For example, GNN.g7208751_000002_002.edit is the identification number of a Genscan-predicted coding sequence, with g7208751 being the GenBank identification number of the sequence to which Genscan was applied. The Genscan-predicted coding sequences may have been edited prior to assembly. (See Example IV.) Alternatively, the identification numbers in column 5 may refer to assemblages of both cDNA and Genscan-predicted exons brought together by an "exon stitching" algorithm. For example, FL1389845_00001 represents a "stitched" sequence in which 1389845 is the identification number of the cluster of sequences to which the algorithm was applied, and 00001 is the number of the prediction generated by the algorithm. (See Example V.) Alternatively, the identification numbers in column 5 may refer to assemblages of both cDNA and Genscan-predicted exons brought together by an "exon-stretching" algorithm. For example, FL2256251_g7708357_000002_g6103629 is the identification

number of a "stretched" sequence, with 2256251 being the Incyte project identification number, g7708357 being the GenBank identification number of the human genomic sequence to which the "exon-stretching" algorithm was applied, and g6103629 being the GenBank identification number of the nearest GenBank protein homolog. (See Example V.) In some cases, Incyte cDNA coverage
5 redundant with the sequence coverage shown in column 5 was obtained to confirm the final consensus polynucleotide sequence, but the relevant Incyte cDNA identification numbers are not shown.

Table 5 shows the representative cDNA libraries for those full length polynucleotide sequences which were assembled using Incyte cDNA sequences. The representative cDNA library is the Incyte cDNA library which is most frequently represented by the Incyte cDNA sequences which were used to
10 assemble and confirm the above polynucleotide sequences. The tissues and vectors which were used to construct the cDNA libraries shown in Table 5 are described in Table 6.

The invention also encompasses PRTS variants. A preferred PRTS variant is one which has at least about 80%, or alternatively at least about 90%, or even at least about 95% amino acid sequence identity to the PRTS amino acid sequence, and which contains at least one functional or structural
15 characteristic of PRTS.

The invention also encompasses polynucleotides which encode PRTS. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:22-42, which encodes PRTS. The polynucleotide sequences of SEQ ID NO:22-42, as presented in the Sequence Listing, embrace the equivalent RNA sequences,
20 wherein occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

The invention also encompasses a variant of a polynucleotide sequence encoding PRTS. In particular, such a variant polynucleotide sequence will have at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to the polynucleotide sequence encoding PRTS. A particular aspect of the invention encompasses a variant of a polynucleotide
25 sequence comprising a sequence selected from the group consisting of SEQ ID NO:22-42 which has at least about 70%, or alternatively at least about 85%, or even at least about 95% polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:22-42. Any one of the polynucleotide variants described above can encode an amino acid sequence which
30 contains at least one functional or structural characteristic of PRTS.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding PRTS, some bearing minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be produced. Thus, the invention contemplates each and every possible variation of polynucleotide sequence that could be made

by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequence of naturally occurring PRTS, and all such variations are to be considered as being specifically disclosed.

Although nucleotide sequences which encode PRTS and its variants are generally capable of hybridizing to the nucleotide sequence of the naturally occurring PRTS under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding PRTS or its derivatives possessing a substantially different codon usage, e.g., inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding PRTS and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

The invention also encompasses production of DNA sequences which encode PRTS and PRTS derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding PRTS or any fragment thereof.

Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID NO:22-42 and fragments thereof under various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511.) Hybridization conditions, including annealing and wash conditions, are described in "Definitions."

Methods for DNA sequencing are well known in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (Applied Biosystems), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies, Gaithersburg MD). Preferably, sequence preparation is automated with machines such as the MICROLAB 2200 liquid transfer system (Hamilton, Reno NV), PTC200 thermal cycler (MJ Research, Watertown MA) and ABI CATALYST 800 thermal cycler (Applied Biosystems). Sequencing is then carried out using either the ABI 373 or 377 DNA sequencing system (Applied Biosystems), the MEGABACE 1000 DNA sequencing system (Molecular Dynamics,

Sunnyvale CA), or other systems known in the art. The resulting sequences are analyzed using a variety of algorithms which are well known in the art. (See, e.g., Ausubel, F.M. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY, unit 7.7; Meyers, R.A. (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853.)

- 5 The nucleic acid sequences encoding PRTS may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) PCR Methods Applic. 2:318-322.)
- 10 Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences. (See, e.g., Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and yeast artificial chromosome DNA. (See, e.g., Lagerstrom, M. et al.
- 15 (1991) PCR Methods Applic. 1:111-119.) In this method, multiple restriction enzyme digestions and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR. Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) Nucleic Acids Res. 19:3055-3060). Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo
- 20 Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 primer analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to
- 25 72°C.

- When screening for full length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5'
- 30 non-transcribed regulatory regions.

 Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the

emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, Applied Biosystems), and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments
5 which may be present in limited amounts in a particular sample.

In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode PRTS may be cloned in recombinant DNA molecules that direct expression of PRTS; or fragments or functional equivalents thereof, in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent
10 amino acid sequence may be produced and used to express PRTS.

The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter PRTS-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic
15 oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

The nucleotides of the present invention may be subjected to DNA shuffling techniques such as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent Number
20 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat. Biotechnol. 17:259-264; and Cramer, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve the biological properties of PRTS, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene variants is produced using PCR-mediated recombination of gene fragments. The library is then
25 subjected to selection or screening procedures that identify those gene variants with the desired properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random point mutations may be recombined, screened, and then reshuffled until the desired properties are
30 optimized. Alternatively, fragments of a given gene may be recombined with fragments of homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

In another embodiment, sequences encoding PRTS may be synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) Nucleic Acids Symp. Ser. 7:215-223; and Horn, T. et al. (1980) Nucleic Acids Symp. Ser. 7:225-232.) Alternatively, PRTS itself or a fragment thereof may be synthesized using chemical methods. For example, peptide
5 synthesis can be performed using various solution-phase or solid-phase techniques. (See, e.g., Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH Freeman, New York NY, pp. 55-60; and Roberge, J.Y. et al. (1995) Science 269:202-204.) Automated synthesis may be achieved using the ABI 431A peptide synthesizer (Applied Biosystems). Additionally, the amino acid sequence of PRTS, or any part thereof, may be altered during direct synthesis and/or combined with sequences
10 from other proteins, or any part thereof, to produce a variant polypeptide or a polypeptide having a sequence of a naturally occurring polypeptide.

The peptide may be substantially purified by preparative high performance liquid chromatography. (See, e.g., Chiez, R.M. and F.Z. Regnier (1990) Methods Enzymol. 182:392-421.) The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing.
15 (See, e.g., Creighton, supra, pp. 28-53.)

In order to express a biologically active PRTS, the nucleotide sequences encoding PRTS or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements include regulatory sequences, such as enhancers, constitutive and
20 inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotide sequences encoding PRTS. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding PRTS. Such signals include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where sequences encoding PRTS and its initiation codon and upstream regulatory sequences are inserted into
25 the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be provided by the vector. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate
30 for the particular host cell system used. (See, e.g., Scharf, D. et al. (1994) Results Probl. Cell Differ. 20:125-162.)

Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding PRTS and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in

vivo genetic recombination. (See, e.g., Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY, ch. 4, 8, and 16-17; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, ch. 9, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences encoding PRTS. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems. (See, e.g., Sambrook, supra; Ausubel, supra; Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509; Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945; Takamatsu, N. (1987) EMBO J. 6:307-311; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196; Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659; and Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.) Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. (See, e.g., Di Nicola, M. et al. (1998) Cancer Gen. Ther. 5(6):350-356; Yu, M. et al. (1993) Proc. Natl. Acad. Sci. USA 90(13):6340-6344; Buller, R.M. et al. (1985) Nature 317(6040):813-815; McGregor, D.P. et al. (1994) Mol. Immunol. 31(3):219-226; and Verma, I.M. and N. Somia (1997) Nature 389:239-242.) The invention is not limited by the host cell employed.

In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding PRTS. For example, routine cloning, subcloning, and propagation of polynucleotide sequences encoding PRTS can be achieved using a multifunctional E. coli vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or PSPORT1 plasmid (Life Technologies). Ligation of sequences encoding PRTS into the vector's multiple cloning site disrupts the *lacZ* gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for in vitro transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster (1989) J. Biol. Chem. 264:5503-5509.) When large quantities of PRTS are needed, e.g. for the production of antibodies, vectors which direct high level expression of PRTS may be used. For example, vectors containing the strong, inducible SP6 or T7 bacteriophage promoter may be used.

Yeast expression systems may be used for production of PRTS. A number of vectors containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH promoters, may be used in the yeast Saccharomyces cerevisiae or Pichia pastoris. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel, 1995, supra; Bitter, G.A. et al. (1987) *Methods Enzymol.* 153:516-544; and Scorer, C.A. et al. (1994) *Bio/Technology* 12:181-184.)

Plant systems may also be used for expression of PRTS. Transcription of sequences encoding PRTS may be driven by viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J.* 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used. (See, e.g., Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984) *Science* 224:838-843; and Winter, J. et al. (1991) *Results Probl. Cell Differ.* 17:85-105.) These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. (See, e.g., The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196.)

In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding PRTS may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain infective virus which expresses PRTS in host cells. (See, e.g., Logan, J. and T. Shenk (1984) *Proc. Natl. Acad. Sci. USA* 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes. (See, e.g., Harrington, J.J. et al. (1997) *Nat. Genet.* 15:345-355.)

For long term production of recombinant proteins in mammalian systems, stable expression of PRTS in cell lines is preferred. For example, sequences encoding PRTS can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to confer resistance to a

selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine phosphoribosyltransferase genes, for use in *tk⁻* and *apr⁻* cells, respectively. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* and *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g., Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14.) Additional selectable genes have been described, e.g., *trpB* and *hisD*, which alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), β glucuronidase and its substrate β -glucuronide, or luciferase and its substrate luciferin may be used. These markers can be used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system. (See, e.g., Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, the presence and expression of the gene may need to be confirmed. For example, if the sequence encoding PRTS is inserted within a marker gene sequence, transformed cells containing sequences encoding PRTS can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding PRTS under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

In general, host cells that contain the nucleic acid sequence encoding PRTS and that express PRTS may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein sequences.

Immunological methods for detecting and measuring the expression of PRTS using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal

antibodies reactive to two non-interfering epitopes on PRTS is preferred, but a competitive binding assay may be employed. These and other assays are well known in the art. (See, e.g., Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press, St. Paul MN, Sect. IV; Coligan, J.E. et al. (1997) Current Protocols in Immunology, Greene Pub. Associates and Wiley-Interscience, New York NY; and Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa NJ.)

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding PRTS include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding PRTS, or any fragments thereof, may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits, such as those provided by Amersham Pharmacia Biotech, Promega (Madison WI), and US Biochemical. Suitable reporter molecules or labels which may be used for ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with nucleotide sequences encoding PRTS may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode PRTS may be designed to contain signal sequences which direct secretion of PRTS through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" or "pro" form of the protein may also be used to specify protein targeting, folding, and/or activity. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38) are available from the American Type Culture Collection (ATCC, Manassas VA) and may be chosen to ensure the correct modification and processing of the foreign protein.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding PRTS may be ligated to a heterologous sequence resulting in translation of a fusion

protein in any of the aforementioned host systems. For example, a chimeric PRTS protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of PRTS activity. Heterologous protein and peptide moieties may also facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metal-chelate resins, respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the PRTS encoding sequence and the heterologous protein sequence, so that PRTS may be cleaved away from the heterologous moiety following purification. Methods for fusion protein expression and purification are discussed in Ausubel (1995, supra, ch. 10). A variety of commercially available kits may also be used to facilitate expression and purification of fusion proteins.

In a further embodiment of the invention, synthesis of radiolabeled PRTS may be achieved in vitro using the TNT rabbit reticulocyte lysate or wheat germ extract system (Promega). These systems couple transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, for example, ^{35}S -methionine.

PRTS of the present invention or fragments thereof may be used to screen for compounds that specifically bind to PRTS. At least one and up to a plurality of test compounds may be screened for specific binding to PRTS. Examples of test compounds include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

In one embodiment, the compound thus identified is closely related to the natural ligand of PRTS, e.g., a ligand or fragment thereof, a natural substrate, a structural or functional mimetic, or a natural binding partner. (See, e.g., Coligan, J.E. et al. (1991) Current Protocols in Immunology 1(2): Chapter 5.) Similarly, the compound can be closely related to the natural receptor to which PRTS binds, or to at least a fragment of the receptor, e.g., the ligand binding site. In either case, the compound can be rationally designed using known techniques. In one embodiment, screening for these compounds involves producing appropriate cells which express PRTS, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or E. coli. Cells expressing PRTS or cell membrane fractions which contain PRTS are then contacted with

a test compound and binding, stimulation, or inhibition of activity of either PRTS or the compound is analyzed.

5 An assay may simply test binding of a test compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. For example, the assay may comprise the steps of combining at least one test compound with PRTS, either in solution or affixed to a solid support, and detecting the binding of PRTS to the compound. Alternatively, the assay may detect or measure binding of a test compound in the presence of a labeled competitor. Additionally, the assay may be carried out using cell-free preparations, chemical libraries, or natural product mixtures, and the test compound(s) may be free in solution or affixed to a
10 solid support.

PRTS of the present invention or fragments thereof may be used to screen for compounds that modulate the activity of PRTS. Such compounds may include agonists, antagonists, or partial or inverse agonists. In one embodiment, an assay is performed under conditions permissive for PRTS activity, wherein PRTS is combined with at least one test compound, and the activity of PRTS in the
15 presence of a test compound is compared with the activity of PRTS in the absence of the test compound. A change in the activity of PRTS in the presence of the test compound is indicative of a compound that modulates the activity of PRTS. Alternatively, a test compound is combined with an in vitro or cell-free system comprising PRTS under conditions suitable for PRTS activity, and the assay is performed. In either of these assays, a test compound which modulates the activity of PRTS may do so
20 indirectly and need not come in direct contact with the test compound. At least one and up to a plurality of test compounds may be screened.

In another embodiment, polynucleotides encoding PRTS or their mammalian homologs may be "knocked out" in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of
25 human disease. (See, e.g., U.S. Patent Number 5,175,383 and U.S. Patent Number 5,767,337.) For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the gene of interest disrupted by a marker gene, e.g., the neomycin phosphotransferase gene (neo; Capecchi, M.R. (1989) Science 244:1288-1292). The vector integrates into the corresponding region of the host genome by
30 homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D. (1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic Acids Res. 25:4323-4330). Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the

resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential therapeutic or toxic agents.

Polynucleotides encoding PRTS may also be manipulated in vitro in ES cells derived from human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell
5 lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

Polynucleotides encoding PRTS can also be used to create "knockin" humanized animals (pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of a
10 polynucleotide encoding PRTS is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and treated with potential pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to overexpress PRTS, e.g., by secreting PRTS in its milk, may also serve as a convenient source
15 of that protein (Janne, J. et al. (1998) Biotechnol. Annu. Rev. 4:55-74).

THERAPEUTICS

PRTS are useful for hydrolyzing peptide bonds. Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of PRTS and proteases. In addition, the expression of PRTS is closely associated with hemic, neurological, reproductive, endocrine,
20 urogenital, diseased, teratocarcinoma, and tumorous tissues,. Therefore, PRTS appears to play a role in gastrointestinal, cardiovascular, autoimmune/inflammatory, cell proliferative, developmental, epithelial, neurological, and reproductive disorders. In the treatment of disorders associated with increased PRTS expression or activity, it is desirable to decrease the expression or activity of PRTS. In the treatment of disorders associated with decreased PRTS expression or activity, it is desirable to
25 increase the expression or activity of PRTS.

Therefore, in one embodiment, PRTS or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PRTS. Examples of such disorders include, but are not limited to, a gastrointestinal disorder, such as
30 dysphagia, peptic esophagitis, esophageal spasm, esophageal stricture, esophageal carcinoma, dyspepsia, indigestion, gastritis, gastric carcinoma, anorexia, nausea, emesis, gastroparesis, antral or pyloric edema, abdominal angina, pyrosis, gastroenteritis, intestinal obstruction, infections of the intestinal tract, peptic ulcer, cholelithiasis, cholecystitis, cholestasis, pancreatitis, pancreatic carcinoma, biliary tract disease, hepatitis, hyperbilirubinemia, cirrhosis, passive congestion of the liver, hepatoma, infectious colitis, ulcerative colitis, ulcerative proctitis, Crohn's disease, Whipple's disease, Mallory-

- Weiss syndrome, colonic carcinoma, colonic obstruction, irritable bowel syndrome, short bowel syndrome, diarrhea, constipation, gastrointestinal hemorrhage, acquired immunodeficiency syndrome (AIDS) enteropathy, jaundice, hepatic encephalopathy, hepatorenal syndrome, hepatic steatosis, hemochromatosis, Wilson's disease, alpha₁-antitrypsin deficiency, Reye's syndrome, primary sclerosing
- 5 cholangitis, liver infarction, portal vein obstruction and thrombosis, centrilobular necrosis, peliosis hepatis, hepatic vein thrombosis, veno-occlusive disease, preeclampsia, eclampsia, acute fatty liver of pregnancy, intrahepatic cholestasis of pregnancy, and hepatic tumors including nodular hyperplasias, adenomas, and carcinomas; a cardiovascular disorder, such as arteriovenous fistula, atherosclerosis, hypertension, vasculitis, Raynaud's disease, aneurysms, arterial dissections, varicose veins,
- 10 thrombophlebitis and phlebothrombosis, vascular tumors, and complications of thrombolysis, balloon angioplasty, vascular replacement, and coronary artery bypass graft surgery, congestive heart failure, ischemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease, degenerative valvular heart disease, calcific aortic valve stenosis, congenitally bicuspid aortic valve, mitral annular calcification, mitral valve prolapse, rheumatic fever and rheumatic heart disease, infective endocarditis,
- 15 nonbacterial thrombotic endocarditis, endocarditis of systemic lupus erythematosus, carcinoid heart disease, cardiomyopathy, myocarditis, pericarditis, neoplastic heart disease, congenital heart disease, and complications of cardiac transplantation; an autoimmune/inflammatory disorder, such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, atherosclerotic plaque rupture,
- 20 autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable
- 25 bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, degradation of articular cartilage, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral,
- 30 bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal

- gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; a developmental disorder, such as renal tubular acidosis, anemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker muscular dystrophy,
- 5 bone resorption, epilepsy, gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spina bifida, anencephaly, craniorachischisis, congenital
- 10 glaucoma, cataract, age-related macular degeneration, and sensorineural hearing loss; an epithelial disorder, such as dyshidrotic eczema, allergic contact dermatitis, keratosis pilaris, melasma, vitiligo, actinic keratosis, basal cell carcinoma, squamous cell carcinoma, seborrheic keratosis, folliculitis, herpes simplex, herpes zoster, varicella, candidiasis, dermatophytosis, scabies, insect bites, cherry angioma, keloid, dermatofibroma, acrochordons, urticaria, transient acantholytic dermatosis, xerosis,
- 15 eczema, atopic dermatitis, contact dermatitis, hand eczema, nummular eczema, lichen simplex chronicus, asteatotic eczema, stasis dermatitis and stasis ulceration, seborrheic dermatitis, psoriasis, lichen planus, pityriasis rosea, impetigo, ecthyma, dermatophytosis, tinea versicolor, warts, acne vulgaris, acne rosacea, pemphigus vulgaris, pemphigus foliaceus, paraneoplastic pemphigus, bullous pemphigoid, herpes gestationis, dermatitis herpetiformis, linear IgA disease, epidermolysis bullosa
- 20 acquisita, dermatomyositis, lupus erythematosus, scleroderma and morphea, erythroderma, alopecia, figurate skin lesions, telangiectasias, hypopigmentation, hyperpigmentation, vesicles/bullae, exanthems, cutaneous drug reactions, papulonodular skin lesions, chronic non-healing wounds, photosensitivity diseases, epidermolysis bullosa simplex, epidermolytic hyperkeratosis, epidermolytic and nonepidermolytic palmoplantar keratoderma, ichthyosis bullosa of Siemens, ichthyosis exfoliativa,
- 25 keratosis palmaris et plantaris, keratosis palmoplantaris, palmoplantar keratoderma, keratosis punctata, Meesmann's corneal dystrophy, pachyonychia congenita, white sponge nevus, steatocystoma multiplex, epidermal nevi/epidermolytic hyperkeratosis type, monilethrix, trichothiodystrophy, chronic hepatitis/cryptogenic cirrhosis, and colorectal hyperplasia; a neurological disorder, such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease,
- 30 Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including

kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system including Down syndrome, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, seasonal affective disorder (SAD), akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, Tourette's disorder, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia; and a reproductive disorder, such as infertility, including tubal disease, ovulatory defects, and endometriosis, a disorder of prolactin production, a disruption of the estrous cycle, a disruption of the menstrual cycle, polycystic ovary syndrome, ovarian hyperstimulation syndrome, an endometrial or ovarian tumor, a uterine fibroid, autoimmune disorders, an ectopic pregnancy, and teratogenesis; cancer of the breast, fibrocystic breast disease, and galactorrhea; a disruption of spermatogenesis, abnormal sperm physiology, cancer of the testis, cancer of the prostate, benign prostatic hyperplasia, prostatitis, Peyronie's disease, impotence, carcinoma of the male breast, and gynecomastia.

In another embodiment, a vector capable of expressing PRTS or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PRTS including, but not limited to, those described above.

In a further embodiment, a composition comprising a substantially purified PRTS in conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PRTS including, but not limited to, those provided above.

In still another embodiment, an agonist which modulates the activity of PRTS may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PRTS including, but not limited to, those listed above.

In a further embodiment, an antagonist of PRTS may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of PRTS. Examples of such disorders include, but are not limited to, those gastrointestinal, cardiovascular, autoimmune/inflammatory, cell proliferative, developmental, epithelial, neurological, and reproductive disorders described above. In one aspect, an antibody which specifically binds PRTS may be used

directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissues which express PRTS.

In an additional embodiment, a vector expressing the complement of the polynucleotide encoding PRTS may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of PRTS including, but not limited to, those described above.

In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

An antagonist of PRTS may be produced using methods which are generally known in the art. In particular, purified PRTS may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind PRTS. Antibodies to PRTS may also be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies (i.e., those which inhibit dimer formation) are generally preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and others may be immunized by injection with PRTS or with any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to PRTS have an amino acid sequence consisting of at least about 5 amino acids, and generally will consist of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are identical to a portion of the amino acid sequence of the natural protein. Short stretches of PRTS amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

Monoclonal antibodies to PRTS may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited

to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique. (See, e.g., Kohler, G. et al. (1975) *Nature* 256:495-497; Kozbor, D. et al. (1985) *J. Immunol. Methods* 81:31-42; Cote, R.J. et al. (1983) *Proc. Natl. Acad. Sci. USA* 80:2026-2030; and Cole, S.P. et al. (1984) *Mol. Cell Biol.* 62:109-120.)

5 In addition, techniques developed for the production of "chimeric antibodies," such as the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984) *Proc. Natl. Acad. Sci. USA* 81:6851-6855; Neuberger, M.S. et al. (1984) *Nature* 312:604-608; and Takeda, S. et al. (1985) *Nature* 314:452-454.) Alternatively, techniques described for the production of single
10 chain antibodies may be adapted, using methods known in the art, to produce PRTS-specific single chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g., Burton, D.R. (1991) *Proc. Natl. Acad. Sci. USA* 88:10134-10137.)

Antibodies may also be produced by inducing in vivo production in the lymphocyte population
15 or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature. (See, e.g., Orlandi, R. et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:3833-3837; Winter, G. et al. (1991) *Nature* 349:293-299.)

Antibody fragments which contain specific binding sites for PRTS may also be generated. For example, such fragments include, but are not limited to, F(ab')₂ fragments produced by pepsin digestion
20 of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D. et al. (1989) *Science* 246:1275-1281.)

Various immunoassays may be used for screening to identify antibodies having the desired
25 specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between PRTS and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering PRTS epitopes is generally used, but a competitive binding assay may also be employed
30 (Pound, supra).

Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for PRTS. Affinity is expressed as an association constant, K_a , which is defined as the molar concentration of PRTS-antibody complex divided by the molar concentrations of free antigen and free antibody under equilibrium conditions. The K_a determined

for a preparation of polyclonal antibodies, which are heterogeneous in their affinities for multiple PRTS epitopes, represents the average affinity, or avidity, of the antibodies for PRTS. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular PRTS epitope, represents a true measure of affinity. High-affinity antibody preparations with K_a ranging from about 10^9 to 10^{12} L/mole are preferred for use in immunoassays in which the PRTS-antibody complex must withstand rigorous manipulations. Low-affinity antibody preparations with K_a ranging from about 10^6 to 10^7 L/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of PRTS, preferably in active form, from the antibody (Catty, D. (1988) Antibodies, Volume I: A Practical Approach, IRL Press, Washington DC; Liddell, J.E. and A. Cryer (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to determine the quality and suitability of such preparations for certain downstream applications. For example, a polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml, preferably 5-10 mg specific antibody/ml, is generally employed in procedures requiring precipitation of PRTS-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines for antibody quality and usage in various applications, are generally available. (See, e.g., Catty, supra, and Coligan et al. supra.)

In another embodiment of the invention, the polynucleotides encoding PRTS, or any fragment or complement thereof, may be used for therapeutic purposes. In one aspect, modifications of gene expression can be achieved by designing complementary sequences or antisense molecules (DNA, RNA, PNA, or modified oligonucleotides) to the coding or regulatory regions of the gene encoding PRTS. Such technology is well known in the art, and antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding PRTS. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totawa NJ.)

In therapeutic use, any gene delivery system suitable for introduction of the antisense sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence complementary to at least a portion of the cellular sequence encoding the target protein. (See, e.g., Slater, J.E. et al. (1998) *J. Allergy Clin. Immunol.* 102(3):469-475; and Scanlon, K.J. et al. (1995) 9(13):1288-1296.) Antisense sequences can also be introduced intracellularly through the use of viral vectors, such as retrovirus and adeno-associated virus vectors. (See, e.g., Miller, A.D. (1990) *Blood* 76:271; Ausubel, supra; Uckert, W. and W. Walther (1994) *Pharmacol. Ther.* 63(3):323-347.) Other gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art. (See, e.g., Rossi, J.J. (1995) *Br. Med. Bull.* 51(1):217-225; Boado, R.J. et

al. (1998) J. Pharm. Sci. 87(11):1308-1315; and Morris, M.C. et al. (1997) Nucleic Acids Res. 25(14):2730-2736.)

In another embodiment of the invention, polynucleotides encoding PRTS may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) Science 288:669-672), severe combined immunodeficiency syndrome associated with an inherited adenosine deaminase (ADA) deficiency (Blaese, R.M. et al. (1995) Science 270:475-480; Bordignon, C. et al. (1995) Science 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) Cell 75:207-216; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:643-666; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:667-703), thalassemias, familial hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal, R.G. (1995) Science 270:404-410; Verma, I.M. and N. Somia (1997) Nature 389:239-242)), (ii) express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) Nature 335:395-396; Poeschla, E. et al. (1996) Proc. Natl. Acad. Sci. USA. 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites, such as Candida albicans and Paracoccidioides brasiliensis; and protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in PRTS expression or regulation causes disease, the expression of PRTS from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

In a further embodiment of the invention, diseases or disorders caused by deficiencies in PRTS are treated by constructing mammalian expression vectors encoding PRTS and introducing these vectors by mechanical means into PRTS-deficient cells. Mechanical transfer technologies for use with cells in vivo or ex vitro include (i) direct DNA microinjection into individual cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and W.F. Anderson (1993) Annu. Rev. Biochem. 62:191-217; Ivics, Z. (1997) Cell 91:501-510; Boulay, J-L. and H. Récipon (1998) Curr. Opin. Biotechnol. 9:445-450).

Expression vectors that may be effective for the expression of PRTS include, but are not limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX vectors (Invitrogen, Carlsbad CA), PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF, PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). PRTS may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus

(RSV), SV40 virus, thymidine kinase (TK), or β -actin genes), (ii) an inducible promoter (e.g., the tetracycline-regulated promoter (Gossen, M. and H. Bujard (1992) *Proc. Natl. Acad. Sci. USA* 89:5547-5551; Gossen, M. et al. (1995) *Science* 268:1766-1769; Rossi, F.M.V. and H.M. Blau (1998) *Curr. Opin. Biotechnol.* 9:451-456), commercially available in the T-REX plasmid (Invitrogen)); the
5 ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and Blau, H.M. *supra*), or (iii) a tissue-specific promoter or the native promoter of the endogenous gene encoding PRTS from a normal individual.

Commercially available liposome transformation kits (e.g., the PERFECT LIPID
10 TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver polynucleotides to target cells in culture and require minimal effort to optimize experimental parameters. In the alternative, transformation is performed using the calcium phosphate method (Graham, F.L. and A.J. Eb (1973) *Virology* 52:456-467), or by electroporation (Neumann, E. et al. (1982) *EMBO J.* 1:841-845). The introduction of DNA to primary cells requires modification of these
15 standardized mammalian transfection protocols.

In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to PRTS expression are treated by constructing a retrovirus vector consisting of (i) the polynucleotide encoding PRTS under the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive
20 element (RRE) along with additional retrovirus *cis*-acting RNA sequences and coding sequences required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) *Proc. Natl. Acad. Sci. USA* 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL) that expresses an envelope gene with a tropism for
25 receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al. (1987) *J. Virol.* 61:1647-1650; Bender, M.A. et al. (1987) *J. Virol.* 61:1639-1646; Adam, M.A. and A.D. Miller (1988) *J. Virol.* 62:3802-3806; Dull, T. et al. (1998) *J. Virol.* 72:8463-8471; Zufferey, R. et al. (1998) *J. Virol.* 72:9873-9880). U.S. Patent Number 5,910,434 to Rigg ("Method for obtaining retrovirus packaging cell lines producing high transducing efficiency retroviral supernatant") discloses a
30 method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference. Propagation of retrovirus vectors, transduction of a population of cells (e.g., CD4⁺ T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) *J. Virol.* 71:7020-7029; Bauer, G. et

al. (1997) Blood 89:2259-2267; Bonyhadi, M.L. (1997) J. Virol. 71:4707-4716; Ranga, U. et al. (1998) Proc. Natl. Acad. Sci. USA 95:1201-1206; Su, L. (1997) Blood 89:2283-2290).

In the alternative, an adenovirus-based gene therapy delivery system is used to deliver polynucleotides encoding PRTS to cells which have one or more genetic abnormalities with respect to the expression of PRTS. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill in the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) Transplantation 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent Number 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999) Annu. Rev. Nutr. 19:511-544 and Verma, I.M. and N. Somia (1997) Nature 18:389:239-242, both incorporated by reference herein.

In another alternative, a herpes-based, gene therapy delivery system is used to deliver polynucleotides encoding PRTS to target cells which have one or more genetic abnormalities with respect to the expression of PRTS. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing PRTS to cells of the central nervous system, for which HSV has a tropism. The construction and packaging of herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) Exp. Eye Res. 169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent Number 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby incorporated by reference. U.S. Patent Number 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under the control of the appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W.F. et al. (1999) J. Virol. 73:519-532 and Xu, H. et al. (1994) Dev. Biol. 163:152-161, hereby incorporated by reference. The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the large herpesvirus genomes, the growth and propagation of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary skill in the art.

In another alternative, an alphavirus (positive, single-stranded RNA virus) vector is used to deliver polynucleotides encoding PRTS to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based on

the SFV genome (Garoff, H. and K.-J. Li (1998) Curr. Opin. Biotechnol. 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full length genomic RNA, resulting in the overproduction of capsid proteins relative to the viral proteins with enzymatic activity (e.g., protease and polymerase). Similarly, inserting the coding sequence for PRTS into the alphavirus genome in place of the capsid-coding region results in the production of a large number of PRTS-coding RNAs and the synthesis of high levels of PRTS in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN) indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) Virology 228:74-83). The wide host range of alphaviruses will allow the introduction of PRTS into a variety of cell types. The specific transduction of a subset of cells in a population may require the sorting of cells prior to transduction. The methods of manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA transfections, and performing alphavirus infections, are well known to those with ordinary skill in the art.

Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, may also be employed to inhibit gene expression. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee, J.E. et al. (1994) in Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing, Mt. Kisco NY, pp. 163-177.) A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. For example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding PRTS.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides, corresponding to the region of the target gene containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of

candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA sequences encoding PRTS. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases.

An additional embodiment of the invention encompasses a method for screening for a compound which is effective in altering expression of a polynucleotide encoding PRTS. Compounds which may be effective in altering expression of a specific polynucleotide may include, but are not limited to, oligonucleotides, antisense oligonucleotides, triple helix-forming oligonucleotides, transcription factors and other polypeptide transcriptional regulators, and non-macromolecular chemical entities which are capable of interacting with specific polynucleotide sequences. Effective compounds may alter polynucleotide expression by acting as either inhibitors or promoters of polynucleotide expression. Thus, in the treatment of disorders associated with increased PRTS expression or activity, a compound which specifically inhibits expression of the polynucleotide encoding PRTS may be therapeutically useful, and in the treatment of disorders associated with decreased PRTS expression or activity, a compound which specifically promotes expression of the polynucleotide encoding PRTS may be therapeutically useful.

At least one, and up to a plurality, of test compounds may be screened for effectiveness in altering expression of a specific polynucleotide. A test compound may be obtained by any method commonly known in the art, including chemical modification of a compound known to be effective in altering polynucleotide expression; selection from an existing, commercially-available or proprietary library of naturally-occurring or non-natural chemical compounds; rational design of a compound based on chemical and/or structural properties of the target polynucleotide; and selection from a

library of chemical compounds created combinatorially or randomly. A sample comprising a polynucleotide encoding PRTS is exposed to at least one test compound thus obtained. The sample may comprise, for example, an intact or permeabilized cell, or an in vitro cell-free or reconstituted biochemical system. Alterations in the expression of a polynucleotide encoding PRTS are assayed by
5 any method commonly known in the art. Typically, the expression of a specific nucleotide is detected by hybridization with a probe having a nucleotide sequence complementary to the sequence of the polynucleotide encoding PRTS. The amount of hybridization may be quantified, thus forming the basis for a comparison of the expression of the polynucleotide both with and without exposure to one or more test compounds. Detection of a change in the expression of a polynucleotide exposed to a
10 test compound indicates that the test compound is effective in altering the expression of the polynucleotide. A screen for a compound effective in altering expression of a specific polynucleotide can be carried out, for example, using a Schizosaccharomyces pombe gene expression system (Atkins, D. et al. (1999) U.S. Patent No. 5,932,435; Arndt, G.M. et al. (2000) Nucleic Acids Res. 28:E15) or a human cell line such as HeLa cell (Clarke, M.L. et al. (2000) Biochem. Biophys. Res. Commun.
15 268:8-13). A particular embodiment of the present invention involves screening a combinatorial library of oligonucleotides (such as deoxyribonucleotides, ribonucleotides, peptide nucleic acids, and modified oligonucleotides) for antisense activity against a specific polynucleotide sequence (Bruice, T.W. et al. (1997) U.S. Patent No. 5,686,242; Bruice, T.W. et al. (2000) U.S. Patent No. 6,022,691).

Many methods for introducing vectors into cells or tissues are available and equally suitable for
20 use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be achieved using methods which are well known in the art. (See, e.g., Goldman, C.K. et al. (1997) Nat. Biotechnol. 15:462-466.)

25 Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as humans, dogs, cats, cows, horses, rabbits, and monkeys.

An additional embodiment of the invention relates to the administration of a composition which generally comprises an active ingredient formulated with a pharmaceutically acceptable excipient.
30 Excipients may include, for example, sugars, starches, celluloses, gums, and proteins. Various formulations are commonly known and are thoroughly discussed in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA). Such compositions may consist of PRTS, antibodies to PRTS, and mimetics, agonists, antagonists, or inhibitors of PRTS.

The compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, pulmonary, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

5 Compositions for pulmonary administration may be prepared in liquid or dry powder form. These compositions are generally aerosolized immediately prior to inhalation by the patient. In the case of small molecules (e.g. traditional low molecular weight organic drugs), aerosol delivery of fast-acting formulations is well-known in the art. In the case of macromolecules (e.g. larger peptides and proteins), recent developments in the field of pulmonary delivery via the alveolar region of the lung have enabled
10 the practical delivery of drugs such as insulin to blood circulation (see, e.g., Patton, J.S. et al., U.S. Patent No. 5,997,848). Pulmonary delivery has the advantage of administration without needle injection, and obviates the need for potentially toxic penetration enhancers.

 Compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of
15 an effective dose is well within the capability of those skilled in the art.

 Specialized forms of compositions may be prepared for direct intracellular delivery of macromolecules comprising PRTS or fragments thereof. For example, liposome preparations containing a cell-impermeable macromolecule may promote cell fusion and intracellular delivery of the macromolecule. Alternatively, PRTS or a fragment thereof may be joined to a short cationic N-
20 terminal portion from the HIV Tat-1 protein. Fusion proteins thus generated have been found to transduce into the cells of all tissues, including the brain, in a mouse model system (Schwarze, S.R. et al. (1999) Science 285:1569-1572).

 For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells, or in animal models such as mice, rats, rabbits, dogs, monkeys,
25 or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

 A therapeutically effective dose refers to that amount of active ingredient, for example PRTS or fragments thereof, antibodies of PRTS, and agonists, antagonists or inhibitors of PRTS, which
30 ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED₅₀ (the dose therapeutically effective in 50% of the population) or LD₅₀ (the dose lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic effects is the therapeutic index, which can be expressed as the LD₅₀/ED₅₀ ratio. Compositions which exhibit large

therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED_{50} with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. Long-acting compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about 0.1 μg to 100,000 μg , up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

In another embodiment, antibodies which specifically bind PRTS may be used for the diagnosis of disorders characterized by expression of PRTS, or in assays to monitor patients being treated with PRTS or agonists, antagonists, or inhibitors of PRTS. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for PRTS include methods which utilize the antibody and a label to detect PRTS in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known in the art and may be used.

A variety of protocols for measuring PRTS, including ELISAs, RIAs, and FACS, are known in the art and provide a basis for diagnosing altered or abnormal levels of PRTS expression. Normal or standard values for PRTS expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, for example, human subjects, with antibodies to PRTS under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, such as photometric means. Quantities of PRTS expressed in subject,

control, and disease samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding PRTS may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantify gene expression in biopsied tissues in which expression of PRTS may be correlated with disease. The diagnostic assay may be used to determine absence, presence, and excess expression of PRTS, and to monitor regulation of PRTS levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding PRTS or closely related molecules may be used to identify nucleic acid sequences which encode PRTS. The specificity of the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification will determine whether the probe identifies only naturally occurring sequences encoding PRTS, allelic variants, or related sequences.

Probes may also be used for the detection of related sequences, and may have at least 50% sequence identity to any of the PRTS encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be derived from the sequence of SEQ ID NO:22-42 or from genomic sequences including promoters, enhancers, and introns of the PRTS gene.

Means for producing specific hybridization probes for DNAs encoding PRTS include the cloning of polynucleotide sequences encoding PRTS or PRTS derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of reporter groups, for example, by radionuclides such as ^{32}P or ^{35}S , or by enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotide sequences encoding PRTS may be used for the diagnosis of disorders associated with expression of PRTS. Examples of such disorders include, but are not limited to, a gastrointestinal disorder, such as dysphagia, peptic esophagitis, esophageal spasm, esophageal stricture, esophageal carcinoma, dyspepsia, indigestion, gastritis, gastric carcinoma, anorexia, nausea, emesis, gastroparesis, antral or pyloric edema, abdominal angina, pyrosis, gastroenteritis, intestinal obstruction, infections of the intestinal tract, peptic ulcer, cholelithiasis, cholecystitis, cholestasis, pancreatitis, pancreatic carcinoma, biliary tract disease, hepatitis, hyperbilirubinemia, cirrhosis, passive congestion of the liver, hepatoma, infectious colitis, ulcerative colitis, ulcerative proctitis, Crohn's disease, Whipple's disease,

Mallory-Weiss syndrome, colonic carcinoma, colonic obstruction, irritable bowel syndrome, short bowel syndrome, diarrhea, constipation, gastrointestinal hemorrhage, acquired immunodeficiency syndrome (AIDS) enteropathy, jaundice, hepatic encephalopathy, hepatorenal syndrome, hepatic steatosis, hemochromatosis, Wilson's disease, α_1 -antitrypsin deficiency, Reye's syndrome, primary sclerosing cholangitis, liver infarction, portal vein obstruction and thrombosis, centrilobular necrosis, peliosis hepatis, hepatic vein thrombosis, veno-occlusive disease, preeclampsia, eclampsia, acute fatty liver of pregnancy, intrahepatic cholestasis of pregnancy, and hepatic tumors including nodular hyperplasias, adenomas, and carcinomas; a cardiovascular disorder, such as arteriovenous fistula, atherosclerosis, hypertension, vasculitis, Raynaud's disease, aneurysms, arterial dissections, varicose veins, thrombophlebitis and phlebothrombosis, vascular tumors, and complications of thrombolysis, balloon angioplasty, vascular replacement, and coronary artery bypass graft surgery, congestive heart failure, ischemic heart disease, angina pectoris, myocardial infarction, hypertensive heart disease, degenerative valvular heart disease, calcific aortic valve stenosis, congenitally bicuspid aortic valve, mitral annular calcification, mitral valve prolapse, rheumatic fever and rheumatic heart disease, infective endocarditis, nonbacterial thrombotic endocarditis, endocarditis of systemic lupus erythematosus, carcinoid heart disease, cardiomyopathy, myocarditis, pericarditis, neoplastic heart disease, congenital heart disease, and complications of cardiac transplantation; an autoimmune/inflammatory disorder, such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, atherosclerotic plaque rupture, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, degradation of articular cartilage, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in

- particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; a developmental disorder, such as renal tubular acidosis, anemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and
- 5 Becker muscular dystrophy, bone resorption, epilepsy, gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary neuropathies such as Charcot-Marie-Tooth disease and neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spina bifida,
- 10 anencephaly, craniorachischisis, congenital glaucoma, cataract, age-related macular degeneration, and sensorineural hearing loss; an epithelial disorder, such as dyshidrotic eczema, allergic contact dermatitis, keratosis pilaris, melasma, vitiligo, actinic keratosis, basal cell carcinoma, squamous cell carcinoma, seborrheic keratosis, folliculitis, herpes simplex, herpes zoster, varicella, candidiasis, dermatophytosis, scabies, insect bites, cherry angioma, keloid, dermatofibroma, acrochordons,
- 15 urticaria, transient acantholytic dermatosis, xerosis, eczema, atopic dermatitis, contact dermatitis, hand eczema, nummular eczema, lichen simplex chronicus, asteatotic eczema, stasis dermatitis and stasis ulceration, seborrheic dermatitis, psoriasis, lichen planus, pityriasis rosea, impetigo, ecthyma, dermatophytosis, tinea versicolor, warts, acne vulgaris, acne rosacea, pemphigus vulgaris, pemphigus foliaceus, paraneoplastic pemphigus, bullous pemphigoid, herpes gestationis, dermatitis herpetiformis,
- 20 linear IgA disease, epidermolysis bullosa acquisita, dermatomyositis, lupus erythematosus, scleroderma and morphea, erythroderma, alopecia, figurate skin lesions, telangiectasias, hypopigmentation, hyperpigmentation, vesicles/bullae, exanthems, cutaneous drug reactions, papulonodular skin lesions, chronic non-healing wounds, photosensitivity diseases, epidermolysis bullosa simplex, epidermolytic hyperkeratosis, epidermolytic and nonepidermolytic palmoplantar keratoderma, ichthyosis bullosa of
- 25 Siemens, ichthyosis exfoliativa, keratosis palmaris et plantaris, keratosis palmoplantaris, palmoplantar keratoderma, keratosis punctata, Meesmann's corneal dystrophy, pachyonychia congenita, white sponge nevus, steatocystoma multiplex, epidermal nevi/epidermolytic hyperkeratosis type, monilethrix, trichothiodystrophy, chronic hepatitis/cryptogenic cirrhosis, and colorectal hyperplasia; a neurological disorder, such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's
- 30 disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion

diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system including Down syndrome, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathies, myasthenia gravis, periodic paralysis, mental disorders including mood, anxiety, and schizophrenic disorders, seasonal affective disorder (SAD), akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, Tourette's disorder, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia; and a reproductive disorder, such as infertility, including tubal disease, ovulatory defects, and endometriosis, a disorder of prolactin production, a disruption of the estrous cycle, a disruption of the menstrual cycle, polycystic ovary syndrome, ovarian hyperstimulation syndrome, an endometrial or ovarian tumor, a uterine fibroid, autoimmune disorders, an ectopic pregnancy, and teratogenesis; cancer of the breast, fibrocystic breast disease, and galactorrhea; a disruption of spermatogenesis, abnormal sperm physiology, cancer of the testis, cancer of the prostate, benign prostatic hyperplasia, prostatitis, Peyronie's disease, impotence, carcinoma of the male breast, and gynecomastia. The polynucleotide sequences encoding PRTS may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and multiformat ELISA-like assays; and in microarrays utilizing fluids or tissues from patients to detect altered PRTS expression. Such qualitative or quantitative methods are well known in the art.

In a particular aspect, the nucleotide sequences encoding PRTS may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences encoding PRTS may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantified and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences encoding PRTS in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

In order to provide a basis for the diagnosis of a disorder associated with expression of PRTS, a normal or standard profile for expression is established. This may be accomplished by combining

body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding PRTS, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used.

- 5 Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

Once the presence of a disorder is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to determine if the level of expression in the
10 patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

With respect to cancer, the presence of an abnormal amount of transcript (either under- or overexpressed) in biopsied tissue from an individual may indicate a predisposition for the development
15 of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Additional diagnostic uses for oligonucleotides designed from the sequences encoding PRTS
20 may involve the use of PCR. These oligomers may be chemically synthesized, generated enzymatically, or produced in vitro. Oligomers will preferably contain a fragment of a polynucleotide encoding PRTS, or a fragment of a polynucleotide complementary to the polynucleotide encoding PRTS, and will be employed under optimized conditions for identification of a specific gene or condition. Oligomers may also be employed under less stringent conditions for detection or quantification of closely related DNA
25 or RNA sequences.

In a particular aspect, oligonucleotide primers derived from the polynucleotide sequences encoding PRTS may be used to detect single nucleotide polymorphisms (SNPs). SNPs are substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease in humans. Methods of SNP detection include, but are not limited to, single-stranded conformation
30 polymorphism (SSCP) and fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from the polynucleotide sequences encoding PRTS are used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for example, from diseased or normal tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause differences in the secondary and tertiary structures of PCR products in single-stranded form, and these differences are detectable

using gel electrophoresis in non-denaturing gels. In fSCCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis methods, termed *in silico* SNP (isSNP), are capable of identifying polymorphisms by comparing the sequence of individual
5 overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass spectrometry using, for example, the high throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

10 Methods which may also be used to quantify the expression of PRTS include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) *J. Immunol. Methods* 159:235-244; Duplaa, C. et al. (1993) *Anal. Biochem.* 212:229-236.) The speed of quantitation of multiple samples may be accelerated by running the assay in a high-throughput format where the oligomer or polynucleotide of
15 interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as elements on a microarray. The microarray can be used in transcript imaging techniques which monitor the relative expression levels of large
20 numbers of genes simultaneously as described below. The microarray may also be used to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, to monitor progression/regression of disease as a function of gene expression, and to develop and monitor the activities of therapeutic agents in the treatment of disease. In particular, this information may be used
25 to develop a pharmacogenomic profile of a patient in order to select the most appropriate and effective treatment regimen for that patient. For example, therapeutic agents which are highly effective and display the fewest side effects may be selected for a patient based on his/her pharmacogenomic profile.

In another embodiment, PRTS, fragments of PRTS, or antibodies specific for PRTS may be used as elements on a microarray. The microarray may be used to monitor or measure protein-protein
30 interactions, drug-target interactions, and gene expression profiles, as described above.

A particular embodiment relates to the use of the polynucleotides of the present invention to generate a transcript image of a tissue or cell type. A transcript image represents the global pattern of gene expression by a particular tissue or cell type. Global gene expression patterns are analyzed by quantifying the number of expressed genes and their relative abundance under given conditions and at a

given time. (See Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, expressly incorporated by reference herein.) Thus a transcript image may be generated by hybridizing the polynucleotides of the present invention or their complements to the totality of transcripts or reverse transcripts of a particular tissue or cell type. In one embodiment, the hybridization takes place in high-throughput format, wherein the polynucleotides of the present invention or their complements comprise a subset of a plurality of elements on a microarray. The resultant transcript image would provide a profile of gene activity.

Transcript images may be generated using transcripts isolated from tissues, cell lines, biopsies, or other biological samples. The transcript image may thus reflect gene expression in vivo, as in the case of a tissue or biopsy sample, or in vitro, as in the case of a cell line.

Transcript images which profile the expression of the polynucleotides of the present invention may also be used in conjunction with in vitro model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental compounds. All compounds induce characteristic gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity (Nuwaysir, E.F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and N.L. Anderson (2000) Toxicol. Lett. 112-113:467-471, expressly incorporated by reference herein). If a test compound has a signature similar to that of a compound with known toxicity, it is likely to share those toxic properties. These fingerprints or signatures are most useful and refined when they contain expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality signature. Even genes whose expression is not altered by any tested compounds are important as well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization procedure is useful for comparison of expression data after treatment with different compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released February 29, 2000, available at <http://www.niehs.nih.gov/oc/news/toxchip.htm>.) Therefore, it is important and desirable in toxicological screening using toxicant signatures to include all expressed gene sequences.

In one embodiment, the toxicity of a test compound is assessed by treating a biological sample containing nucleic acids with the test compound. Nucleic acids that are expressed in the treated biological sample are hybridized with one or more probes specific to the polynucleotides of the present invention, so that transcript levels corresponding to the polynucleotides of the present

invention may be quantified. The transcript levels in the treated biological sample are compared with levels in an untreated biological sample. Differences in the transcript levels between the two samples are indicative of a toxic response caused by the test compound in the treated sample.

Another particular embodiment relates to the use of the polypeptide sequences of the present invention to analyze the proteome of a tissue or cell type. The term proteome refers to the global pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome can be subjected individually to further analysis. Proteome expression patterns, or profiles, are analyzed by quantifying the number of expressed proteins and their relative abundance under given conditions and at a given time. A profile of a cell's proteome may thus be generated by separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the separation is achieved using two-dimensional gel electrophoresis, in which proteins from a sample are separated by isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson, *supra*). The proteins are visualized in the gel as discrete and uniquely positioned spots, typically by staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical density of each protein spot is generally proportional to the level of the protein in the sample. The optical densities of equivalently positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are compared to identify any changes in protein spot density related to the treatment. The proteins in the spots are partially sequenced using, for example, standard methods employing chemical or enzymatic cleavage followed by mass spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of at least 5 contiguous amino acid residues, to the polypeptide sequences of the present invention. In some cases, further sequence data may be obtained for definitive protein identification.

A proteomic profile may also be generated using antibodies specific for PRTS to quantify the levels of PRTS expression. In one embodiment, the antibodies are used as elements on a microarray, and protein expression levels are quantified by exposing the microarray to the sample and detecting the levels of protein bound to each array element (Lueking, A. et al. (1999) *Anal. Biochem.* 270:103-111; Mendoz, I. G. et al. (1999) *Biotechniques* 27:778-788). Detection may be performed by a variety of methods known in the art, for example, by reacting the proteins in the sample with a thiol- or amino-reactive fluorescent compound and detecting the amount of fluorescence bound at each array element.

Toxicant signatures at the proteome level are also useful for toxicological screening, and should be analyzed in parallel with toxicant signatures at the transcript level. There is a poor correlation between transcript and protein abundances for some proteins in some tissues (Anderson, N.L. and J. Seilhamer (1997) *Electrophoresis* 18:533-537), so proteome toxicant signatures may be useful in the

analysis of compounds which do not significantly affect the transcript image, but which alter the proteomic profile. In addition, the analysis of transcripts in body fluids is difficult, due to rapid degradation of mRNA, so proteomic profiling may be more reliable and informative in such cases.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins that are expressed in the treated biological sample are separated so that the amount of each protein can be quantified. The amount of each protein is compared to the amount of the corresponding protein in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample. Individual proteins are identified by sequencing the amino acid residues of the individual proteins and comparing these partial sequences to the polypeptides of the present invention.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins from the biological sample are incubated with antibodies specific to the polypeptides of the present invention. The amount of protein recognized by the antibodies is quantified. The amount of protein in the treated biological sample is compared with the amount in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. USA 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. USA 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.) Various types of microarrays are well known and thoroughly described in DNA Microarrays: A Practical Approach, M. Schena, ed. (1999) Oxford University Press, London, hereby expressly incorporated by reference.

In another embodiment of the invention, nucleic acid sequences encoding PRTS may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. Either coding or noncoding sequences may be used, and in some instances, noncoding sequences may be preferable over coding sequences. For example, conservation of a coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.) Once mapped, the nucleic acid sequences of the invention may be used to develop genetic

linkage maps, for example, which correlate the inheritance of a disease state with the inheritance of a particular chromosome region or restriction fragment length polymorphism (RFLP). (See, for example, Lander, E.S. and D. Botstein (1986) Proc. Natl. Acad. Sci. USA 83:7353-7357.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical and genetic map data. (See, e.g., Heinz-Ulrich, et al. (1995) in Meyers, supra, pp. 965-968.) Examples of genetic map data can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) World Wide Web site. Correlation between the location of the gene encoding PRTS on a physical map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder and thus may further positional cloning efforts.

10 In situ hybridization of chromosomal preparations and physical mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the exact chromosomal locus is not known. This information is valuable to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the gene or genes responsible for a disease or syndrome have been crudely localized by genetic linkage to a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequence of the instant invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier, or affected individuals.

20 In another embodiment of the invention, PRTS, its catalytic or immunogenic fragments, or oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes between PRTS and the agent being tested may be measured.

25 Another technique for drug screening provides for high throughput screening of compounds having suitable binding affinity to the protein of interest. (See, e.g., Geysen, et al. (1984) PCT application WO84/03564.) In this method, large numbers of different small test compounds are synthesized on a solid substrate. The test compounds are reacted with PRTS, or fragments thereof, and washed. Bound PRTS is then detected by methods well known in the art. Purified PRTS can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

30 In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding PRTS specifically compete with a test compound for binding PRTS. In

this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRTS.

In additional embodiments, the nucleotide sequences which encode PRTS may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, including U.S. Ser. No. 60/212,336, U.S. Ser. No. 60/213,995, U.S. Ser. No. 60/215,396, U.S. Ser. No. 60/216,821, and U.S. Ser. No. 60/218,946, are hereby expressly incorporated by reference.

EXAMPLES

I. Construction of cDNA Libraries

Incyte cDNAs were derived from cDNA libraries described in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA) and shown in Table 4, column 5. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In some cases, RNA was treated with DNase. For most libraries, poly(A)+ RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles (QIAGEN, Chatsworth CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene) or SUPERScript plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, *supra*, units 5.1-6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic

oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUESCRIPT plasmid (Stratagene), PSPO1 plasmid (Life Technologies), PCDNA2.1 plasmid (Invitrogen, Carlsbad CA), PBK-CMV plasmid (Stratagene), or pINCY (Incyte Genomics, Palo Alto CA), or derivatives thereof. Recombinant plasmids were transformed into competent *E. coli* cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectroMAX DH10B from Life Technologies.

II. Isolation of cDNA Clones

Plasmids obtained as described in Example I were recovered from host cells by *in vivo* excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8 Plus Plasmid, QIAWELL 8 Ultra Plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Eugene OR) and a FLUOROSKAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

Incyte cDNA recovered in plasmids as described in Example II were sequenced as follows. Sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 (Applied Biosystems) thermal cycler or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific) or the MICROLAB 2200 (Hamilton) liquid transfer system. cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI

PRISM 373 or 377 sequencing system (Applied Biosystems) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, supra, unit 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example VIII.

The polynucleotide sequences derived from Incyte cDNAs were validated by removing vector, linker, and poly(A) sequences and by masking ambiguous bases, using algorithms and programs based on BLAST, dynamic programming, and dinucleotide nearest neighbor analysis. The Incyte cDNA sequences or translations thereof were then queried against a selection of public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS, PRINTS, DOMO, PRODOM, and hidden Markov model (HMM)-based protein family databases such as PFAM. (HMM is a probabilistic approach which analyzes consensus primary structures of gene families. See, for example, Eddy, S.R. (1996) *Curr. Opin. Struct. Biol.* 6:361-365.) The queries were performed using programs based on BLAST, FASTA, BLIMPS, and HMMER. The Incyte cDNA sequences were assembled to produce full length polynucleotide sequences. Alternatively, GenBank cDNAs, GenBank ESTs, stitched sequences, stretched sequences, or Genscan-predicted coding sequences (see Examples IV and V) were used to extend Incyte cDNA assemblages to full length. Assembly was performed using programs based on Phred, Phrap, and Consed, and cDNA assemblages were screened for open reading frames using programs based on GeneMark, BLAST, and FASTA. The full length polynucleotide sequences were translated to derive the corresponding full length polypeptide sequences. Alternatively, a polypeptide of the invention may begin at any of the methionine residues of the full length translated polypeptide. Full length polypeptide sequences were subsequently analyzed by querying against databases such as the GenBank protein databases (genpept), SwissProt, BLOCKS, PRINTS, DOMO, PRODOM, Prosite, and hidden Markov model (HMM)-based protein family databases such as PFAM. Full length polynucleotide sequences are also analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments are generated using default parameters specified by the CLUSTAL algorithm as incorporated into the MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.

Table 7 summarizes the tools, programs, and algorithms used for the analysis and assembly of Incyte cDNA and full length sequences and provides applicable descriptions, references, and threshold parameters. The first column of Table 7 shows the tools, programs, and algorithms used, the second column provides brief descriptions thereof, the third column presents appropriate references, all of

which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score or the lower the probability value, the greater the identity between two sequences).

5 The programs described above for the assembly and analysis of full length polynucleotide and polypeptide sequences were also used to identify polynucleotide sequence fragments from SEQ ID NO:22-42. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies are described in Table 4, column 4.

IV. Identification and Editing of Coding Sequences from Genomic DNA

10 Putative proteases were initially identified by running the Genscan gene identification program against public genomic sequence databases (e.g., gbpri and gbhtg). Genscan is a general-purpose gene identification program which analyzes genomic DNA sequences from a variety of organisms (See Burge, C. and S. Karlin (1997) J. Mol. Biol. 268:78-94, and Burge, C. and S. Karlin (1998) Curr. Opin. Struct. Biol. 8:346-354). The program concatenates predicted exons to form an assembled
15 cDNA sequence extending from a methionine to a stop codon. The output of Genscan is a FASTA database of polynucleotide and polypeptide sequences. The maximum range of sequence for Genscan to analyze at once was set to 30 kb. To determine which of these Genscan predicted cDNA sequences encode proteases, the encoded polypeptides were analyzed by querying against PFAM models for proteases. Potential proteases were also identified by homology to Incyte cDNA sequences that had
20 been annotated as proteases. These selected Genscan-predicted sequences were then compared by BLAST analysis to the genpept and gbpri public databases. Where necessary, the Genscan-predicted sequences were then edited by comparison to the top BLAST hit from genpept to correct errors in the sequence predicted by Genscan, such as extra or omitted exons. BLAST analysis was also used to find any Incyte cDNA or public cDNA coverage of the Genscan-predicted sequences, thus providing
25 evidence for transcription. When Incyte cDNA coverage was available, this information was used to correct or confirm the Genscan predicted sequence. Full length polynucleotide sequences were obtained by assembling Genscan-predicted coding sequences with Incyte cDNA sequences and/or public cDNA sequences using the assembly process described in Example III. Alternatively, full length polynucleotide sequences were derived entirely from edited or unedited Genscan-predicted coding
30 sequences.

V. Assembly of Genomic Sequence Data with cDNA Sequence Data

"Stitched" Sequences

Partial cDNA sequences were extended with exons predicted by the Genscan gene identification program described in Example IV. Partial cDNAs assembled as described in Example III were mapped

to genomic DNA and parsed into clusters containing related cDNAs and Genscan exon predictions from one or more genomic sequences. Each cluster was analyzed using an algorithm based on graph theory and dynamic programming to integrate cDNA and genomic information, generating possible splice variants that were subsequently confirmed, edited, or extended to create a full length sequence.

5 Sequence intervals in which the entire length of the interval was present on more than one sequence in the cluster were identified, and intervals thus identified were considered to be equivalent by transitivity. For example, if an interval was present on a cDNA and two genomic sequences, then all three intervals were considered to be equivalent. This process allows unrelated but consecutive genomic sequences to be brought together, bridged by cDNA sequence. Intervals thus identified were then "stitched" together
10 by the stitching algorithm in the order that they appear along their parent sequences to generate the longest possible sequence, as well as sequence variants. Linkages between intervals which proceed along one type of parent sequence (cDNA to cDNA or genomic sequence to genomic sequence) were given preference over linkages which change parent type (cDNA to genomic sequence). The resultant stitched sequences were translated and compared by BLAST analysis to the genpept and gbpi public
15 databases. Incorrect exons predicted by Genscan were corrected by comparison to the top BLAST hit from genpept. Sequences were further extended with additional cDNA sequences, or by inspection of genomic DNA, when necessary.

"Stretched" Sequences

Partial DNA sequences were extended to full length with an algorithm based on BLAST
20 analysis. First, partial cDNAs assembled as described in Example III were queried against public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases using the BLAST program. The nearest GenBank protein homolog was then compared by BLAST analysis to either Incyte cDNA sequences or GenScan exon predicted sequences described in Example IV. A chimeric protein was generated by using the resultant high-scoring segment pairs (HSPs) to map the
25 translated sequences onto the GenBank protein homolog. Insertions or deletions may occur in the chimeric protein with respect to the original GenBank protein homolog. The GenBank protein homolog, the chimeric protein, or both were used as probes to search for homologous genomic sequences from the public human genome databases. Partial DNA sequences were therefore "stretched" or extended by the addition of homologous genomic sequences. The resultant stretched sequences were examined to
30 determine whether it contained a complete gene.

VI. Chromosomal Mapping of PRTS Encoding Polynucleotides

The sequences which were used to assemble SEQ ID NO:22-42 were compared with sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these databases that matched

SEQ ID NO:22-42 were assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as Phrap (Table 7). Radiation hybrid and genetic mapping data available from public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for Genome Research (WIGR), and Généthon were used to determine if any of the clustered sequences
5 had been previously mapped. Inclusion of a mapped sequence in a cluster resulted in the assignment of all sequences of that cluster, including its particular SEQ ID NO:, to that map location.

Map locations are represented by ranges, or intervals, of human chromosomes. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between
10 chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Généthon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters. Human genome maps and other resources available to the public, such as the NCBI "GeneMap'99" World Wide Web site
15 (<http://www.ncbi.nlm.nih.gov/genemap/>), can be employed to determine if previously identified disease genes map within or in proximity to the intervals indicated above.

In this manner, SEQ ID NO:25 was mapped to chromosome 5 within the interval from 69.60 to 76.50 centiMorgans. SEQ ID NO:28 was mapped to chromosome 16 within the interval from 81.80 to 84.40 centiMorgans.

20 VII. Analysis of Polynucleotide Expression

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; Ausubel (1995) supra, ch. 4 and 16.)

25 Analogous computer techniques applying BLAST were used to search for identical or related molecules in cDNA databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

30

$$\frac{\text{BLAST Score} \times \text{Percent Identity}}{5 \times \text{minimum \{length(Seq. 1), length(Seq. 2)\}}}$$

The product score takes into account both the degree of similarity between two sequences and the length
35 of the sequence match. The product score is a normalized value between 0 and 100, and is calculated

as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the entire length of the shorter of the two sequences being compared. A product score of 70 is produced either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or 79% identity and 100% overlap.

Alternatively, polynucleotide sequences encoding PRTS are analyzed with respect to the tissue sources from which they were derived. For example, some full length sequences are assembled, at least in part, with overlapping Incyte cDNA sequences (see Example III). Each cDNA sequence is derived from a cDNA library constructed from a human tissue. Each human tissue is classified into one of the following organ/tissue categories: cardiovascular system; connective tissue; digestive system; embryonic structures; endocrine system; exocrine glands; genitalia, female; genitalia, male; germ cells; hemic and immune system; liver; musculoskeletal system; nervous system; pancreas; respiratory system; sense organs; skin; stomatognathic system; unclassified/mixed; or urinary tract. The number of libraries in each category is counted and divided by the total number of libraries across all categories. Similarly, each human tissue is classified into one of the following disease/condition categories: cancer, cell line, developmental, inflammation, neurological, trauma, cardiovascular, pooled, and other, and the number of libraries in each category is counted and divided by the total number of libraries across all categories. The resulting percentages reflect the tissue- and disease-specific expression of cDNA encoding PRTS. cDNA sequences and cDNA library/tissue information are found in the LIFESEQ GOLD database (Incyte Genomics, Palo Alto CA).

VIII. Extension of PRTS Encoding Polynucleotides

Full length polynucleotide sequences were also produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this fragment. One primer was synthesized to initiate 5' extension of the known fragment, and the other primer was synthesized to initiate 3' extension of the known fragment. The initial primers were designed using OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

Selected human cDNA libraries were used to extend the sequence. If more than one extension was necessary or desired, additional or nested sets of primers were designed.

High fidelity amplification was obtained by PCR using methods well known in the art. PCR was performed in 96-well plates using the PTC-200 thermal cycler (MJ Research, Inc.). The reaction mix contained DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+} , $(NH_4)_2SO_4$, and 2-mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 5 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ were as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well was determined by dispensing 100 μ l PICOGREEN quantitation reagent (0.25% (v/v) PICOGREEN; Molecular Probes, Eugene OR) dissolved in 1X TE and 0.5 μ l of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar, Acton MA), allowing the DNA to bind to the reagent. The plate was scanned in a Fluoroskan II (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 μ l to 10 μ l aliquot of the reaction mixture was analyzed by electrophoresis on a 1 % agarose gel to determine which reactions were successful in extending the sequence.

The extended nucleotides were desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides were separated on low concentration (0.6 to 0.8%) agarose gels, fragments were excised, and agar digested with Agar ACE (Promega). Extended clones were religated using T4 ligase (New England Biolabs, Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent *E. coli* cells. Transformed cells were selected on antibiotic-containing media, and individual colonies were picked and cultured overnight at 37°C in 384-well plates in LB/2x carb liquid media.

The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries were reamplified

using the same conditions as described above. Samples were diluted with 20% dimethylsulfoxide (1:2, v/v); and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems).

- 5 In like manner, full length polynucleotide sequences are verified using the above procedure or are used to obtain 5' regulatory sequences using the above procedure along with oligonucleotides designed for such extension, and an appropriate genomic library.

IX. Labeling and Use of Individual Hybridization Probes

- Hybridization probes derived from SEQ ID NO:22-42 are employed to screen cDNAs, genomic
10 DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 μ Ci of [γ - 32 P] adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase (DuPont NEN, Boston
15 MA). The labeled oligonucleotides are substantially purified using a SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech). An aliquot containing 10^7 counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

- 20 The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under conditions of up to, for example, 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. Hybridization patterns are visualized using autoradiography or an alternative imaging means and
25 compared.

X. Microarrays

- The linkage or synthesis of array elements upon a microarray can be achieved utilizing photolithography, piezoelectric printing (ink-jet printing, See, e.g., Baldeschweiler, supra.), mechanical microspotting technologies, and derivatives thereof. The substrate in each of the aforementioned
30 technologies should be uniform and solid with a non-porous surface (Schena (1999), supra). Suggested substrates include silicon, silica, glass slides, glass chips, and silicon wafers. Alternatively, a procedure analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be produced using available methods and machines well known to those of ordinary skill in the art and may

contain any appropriate number of elements. (See, e.g., Schena, M. et al. (1995) *Science* 270:467-470; Shalon, D. et al. (1996) *Genome Res.* 6:639-645; Marshall, A. and J. Hodgson (1998) *Nat. Biotechnol.* 16:27-31.)

Full length cDNAs, Expressed Sequence Tags (ESTs), or fragments or oligomers thereof may
5 comprise the elements of the microarray. Fragments or oligomers suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). The array elements are hybridized with polynucleotides in a biological sample. The polynucleotides in the biological sample are conjugated to a fluorescent label or other molecular tag for ease of detection. After hybridization, nonhybridized nucleotides from the biological sample are removed, and a
10 fluorescence scanner is used to detect hybridization at each array element. Alternatively, laser desorption and mass spectrometry may be used for detection of hybridization. The degree of complementarity and the relative abundance of each polynucleotide which hybridizes to an element on the microarray may be assessed. In one embodiment, microarray preparation and usage is described in detail below.

15 Tissue or Cell Sample Preparation

Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and poly(A)⁺ RNA is purified using the oligo-(dT) cellulose method. Each poly(A)⁺ RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/ μ l oligo-(dT) primer (21mer), 1X first strand buffer, 0.03 units/ μ l RNase inhibitor, 500 μ M dATP, 500 μ M dGTP, 500 μ M dTTP, 40 μ M
20 dCTP, 40 μ M dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Pharmacia Biotech). The reverse transcription reaction is performed in a 25 ml volume containing 200 ng poly(A)⁺ RNA with GEMBRIGHT kits (Incyte). Specific control poly(A)⁺ RNAs are synthesized by in vitro transcription from non-coding yeast genomic DNA. After incubation at 37°C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and
25 incubated for 20 minutes at 85°C to stop the reaction and degrade the RNA. Samples are purified using two successive CHROMA SPIN 30 gel filtration spin columns (CLONTECH Laboratories, Inc. (CLONTECH), Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The sample is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and
30 resuspended in 14 μ l 5X SSC/0.2% SDS.

Microarray Preparation

Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are

amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5 µg. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Pharmacia Biotech).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR Scientific Products Corporation (VWR), West Chester PA), washed extensively in distilled water, and coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a 110°C oven.

Array elements are applied to the coated glass substrate using a procedure described in US Patent No. 5,807,522, incorporated herein by reference. 1 µl of the array element DNA, at an average concentration of 100 ng/µl, is loaded into the open capillary printing element by a high-speed robotic apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate buffered saline (PBS) (Tropix, Inc., Bedford MA) for 30 minutes at 60°C followed by washes in 0.2% SDS and distilled water as before.

Hybridization

Hybridization reactions contain 9 µl of sample mixture consisting of 0.2 µg each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The sample mixture is heated to 65°C for 5 minutes and is aliquoted onto the microarray surface and covered with an 1.8 cm² coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly larger than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140 µl of 5X SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60°C. The arrays are washed for 10 min at 45°C in a first wash buffer (1X SSC, 0.1% SDS), three times for 10 minutes each at 45°C in a second wash buffer (0.1X SSC), and dried.

Detection

Reporter-labeled hybridization complexes are detected with a microscope equipped with an Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a resolution of 20 micrometers.

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially. Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477, Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate filters positioned between the array and the photomultiplier tubes are used to filter the signals. The
5 emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source, although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

The sensitivity of the scans is typically calibrated using the signal intensity generated by a cDNA control species added to the sample mixture at a known concentration. A specific location on
10 the array contains a complementary DNA sequence, allowing the intensity of the signal at that location to be correlated with a weight ratio of hybridizing species of 1:100,000. When two samples from different sources (e.g., representing test and control cells), each labeled with a different fluorophore, are hybridized to a single array for the purpose of identifying genes that are differentially expressed, the calibration is done by labeling samples of the calibrating cDNA with the two
15 fluorophores and adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital (A/D) conversion board (Analog Devices, Inc., Norwood MA) installed in an IBM-compatible PC computer. The digitized data are displayed as an image where the signal intensity is mapped using a linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high
20 signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping emission spectra) between the fluorophores using each fluorophore's emission spectrum.

A grid is superimposed over the fluorescence signal image such that the signal from each spot is centered in each element of the grid. The fluorescence signal within each element is then integrated
25 to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte).

XI. Complementary Polynucleotides

Sequences complementary to the PRTS-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring PRTS. Although use of oligonucleotides
30 comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of PRTS. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is
35 designed to prevent ribosomal binding to the PRTS-encoding transcript.

XII. Expression of PRTS

Expression and purification of PRTS is achieved using bacterial or virus-based expression systems. For expression of PRTS in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription.

- 5 Examples of such promoters include, but are not limited to, the *trp-lac (tac)* hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express PRTS upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of PRTS in eukaryotic cells is achieved by infecting insect or mammalian cell lines with
- 10 recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding PRTS by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect
- 15 cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945.)

- In most expression systems, PRTS is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step,
- 20 affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from PRTS at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification
- 25 using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, ch. 10 and 16). Purified PRTS obtained by these methods can be used directly in the assays shown in Examples XVI, XVII, XVIII, and XIX, where applicable.

30 XIII. Functional Assays

PRTS function is assessed by expressing the sequences encoding PRTS at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include PCMV SPORT (Life Technologies) and PCR3.1 (Invitrogen, Carlsbad CA), both of which

contain the cytomegalovirus promoter. 5-10 μ g of recombinant vector are transiently transfected into a human cell line, for example, an endothelial or hematopoietic cell line, using either liposome formulations or electroporation. 1-2 μ g of an additional plasmid containing sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M.G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of PRTS on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding PRTS and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding PRTS and other genes of interest can be analyzed by northern analysis or microarray techniques.

XIV. Production of PRTS Specific Antibodies

PRTS substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the PRTS amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, supra, ch. 11.)

Typically, oligopeptides of about 15 residues in length are synthesized using an ABI 431A peptide synthesizer (Applied Biosystems) using FMOC chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, 1995, *supra*.) Rabbits are immunized with the
5 oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide and anti-PRTS activity by, for example, binding the peptide or PRTS to a substrate, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

XV. Purification of Naturally Occurring PRTS Using Specific Antibodies

Naturally occurring or recombinant PRTS is substantially purified by immunoaffinity
10 chromatography using antibodies specific for PRTS. An immunoaffinity column is constructed by covalently coupling anti-PRTS antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing PRTS are passed over the immunoaffinity column, and the column is washed
15 under conditions that allow the preferential absorbance of PRTS (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/PRTS binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and PRTS is collected.

XVI. Identification of Molecules Which Interact with PRTS

PRTS, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent.
20 (See, e.g., Bolton A.E. and W.M. Hunter (1973) Biochem. J. 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled PRTS, washed, and any wells with labeled PRTS complex are assayed. Data obtained using different concentrations of PRTS are used to calculate values for the number, affinity, and association of PRTS with the candidate
25 molecules.

Alternatively, molecules interacting with PRTS are analyzed using the yeast two-hybrid system as described in Fields, S. and O. Song (1989) Nature 340:245-246, or using commercially available kits based on the two-hybrid system, such as the MATCHMAKER system (Clontech).

PRTS may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT)
30 which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent No. 6,057,101).

XVII. Demonstration of PRTS Activity

Protease activity is measured by the hydrolysis of appropriate synthetic peptide substrates conjugated with various chromogenic molecules in which the degree of hydrolysis is quantified by spectrophotometric (or fluorometric) absorption of the released chromophore (Beynon, R.J. and J.S. Bond (1994) Proteolytic Enzymes: A Practical Approach, Oxford University Press, New York NY, pp.25-55). Peptide substrates are designed according to the category of protease activity as endopeptidase (serine, cysteine, aspartic proteases, or metalloproteases), aminopeptidase (leucine aminopeptidase), or carboxypeptidase (carboxypeptidases A and B, procollagen C-proteinase). Commonly used chromogens are 2-naphthylamine, 4-nitroaniline, and furylacrylic acid. For example, arginine- β -naphthylamide can be used as a substrate for SEQ ID NO:3 (Fukasawa, K.M. et al. (1996) *J. Biol. Chem.* 271:30731-30735) and 4-phenylazobenzoyloxycarbonyl-Pro-Leu-Gly-Pro-D-Arg can be used as a substrate for SEQ ID NO:4. In an alternative example, a substrate for SEQ ID NO:9 would be 7-amino-4-trifluoromethyl coumarin-Phe-Pro-AFC. Assays are performed at ambient temperature and contain an aliquot of the enzyme and the appropriate substrate in a suitable buffer. Reactions are carried out in an optical cuvette, and the increase/decrease in absorbance of the chromogen released during hydrolysis of the peptide substrate is measured. The change in absorbance is proportional to the enzyme activity in the assay.

An alternate assay for ubiquitin hydrolase activity measures the hydrolysis of a ubiquitin precursor. The assay is performed at ambient temperature and contains an aliquot of PRTS and the appropriate substrate in a suitable buffer. For SEQ ID NO:1, chemically synthesized human ubiquitin-valine may be used as substrate. Cleavage of the C-terminal valine residue from the substrate is monitored by capillary electrophoresis (Franklin, K. et al. (1997) *Anal. Biochem.* 247:305-309).

Alternatively, the ubiquitin protease activity of SEQ ID NO:5 can be measured using the method of Sloper-Mould et al. ((1999) *J. Biol. Chem.* 274:26878-26884). Aliquots of PRTS are incubated with 5 μ l [35 S]-labeled ubiquitin-GST fusion substrate for 1 hour at 37 °C in an appropriate buffer. Samples are resolved by electrophoresis on a 12% SDS-PAGE gel. Ubiquitin cleavage is monitored by fluorography of the gel.

Alternatively, the activity of SEQ ID NO:10, for example, can be measured by the method of Colige et al. (1999, *J. Biol. Chem.* 270:16724-16730). An aliquot of PRTS is incubated with amino procollagen type I substrate radioactively labeled only in the propeptide in a 250 μ l reaction containing 50 mM sodium cacodylate, pH 7.5, 200 mM KCl, 2 mM CaCl₂, 2.5 mM NEM, 0.5 mM PMSF, and 0.02% Brij (standard assay buffer). After 16 h at 26 °C, the reaction is stopped by adding 50 μ l of EDTA solution (0.2 M EDTA, pH 8, 0.5% SDS, 0.5 M DTT) and 300 μ l of 99% ethanol. The samples are kept for 30 min at 4 °C and centrifuged for 30 min at 9500 g. Collagen and uncleaved

radioactive pN-collagen substrate are pelleted, whereas the freed amino propeptides remained in solution. An aliquot of the supernatant is assayed by liquid scintillation spectrometry.

In the alternative, an assay for protease activity takes advantage of fluorescence resonance energy transfer (FRET) that occurs when one donor and one acceptor fluorophore with an appropriate spectral overlap are in close proximity. A flexible peptide linker containing a cleavage site specific for PRTS is fused between a red-shifted variant (RSGFP4) and a blue variant (BFP5) of Green Fluorescent Protein. This fusion protein has spectral properties that suggest energy transfer is occurring from BFP5 to RSGFP4. When the fusion protein is incubated with PRTS, the substrate is cleaved, and the two fluorescent proteins dissociate. This is accompanied by a marked decrease in energy transfer which is quantified by comparing the emission spectra before and after the addition of PRTS (Mitra, R.D. et al. (1996) *Gene* 173:13-17). This assay can also be performed in living cells. In this case the fluorescent substrate protein is expressed constitutively in cells and PRTS is introduced on an inducible vector so that FRET can be monitored in the presence and absence of PRTS (Sagot, I. et al. (1999) *FEBS Lett.* 447:53-57).

In yet another alternative, an assay for PRTS dipeptidase activity measures the hydrolysis activity of PRTS on a variety of dipeptides such as leukotriene D4 (Kozak, E. and S. Tate (1982) *J. Biol. Chem.* 257:6322-6327), or hydrolysis of the beta-lactam ring of antibiotics such as penum and carbapenem (Campbell et al., (1984) *J. Biol. Chem.* 259:14586-14590).

XVIII. Identification of PRTS Substrates

Phage display libraries can be used to identify optimal substrate sequences for PRTS. A random hexamer followed by a linker and a known antibody epitope is cloned as an N-terminal extension of gene III in a filamentous phage library. Gene III codes for a coat protein, and the epitope will be displayed on the surface of each phage particle. The library is incubated with PRTS under proteolytic conditions so that the epitope will be removed if the hexamer codes for a PRTS cleavage site. An antibody that recognizes the epitope is added along with immobilized protein A. Uncleaved phage, which still bear the epitope, are removed by centrifugation. Phage in the supernatant are then amplified and undergo several more rounds of screening. Individual phage clones are then isolated and sequenced. Reaction kinetics for these peptide substrates can be studied using an assay in Example XVII, and an optimal cleavage sequence can be derived (Ke, S.H. et al. (1997) *J. Biol. Chem.* 272:16603-16609).

To screen for in vivo PRTS substrates, this method can be expanded to screen a cDNA expression library displayed on the surface of phage particles (T7SELECT 10-3 Phage display vector, Novagen, Madison WI) or yeast cells (pYD1 yeast display vector kit, Invitrogen, Carlsbad CA). In this case, entire cDNAs are fused between Gene III and the appropriate epitope.

XIX. Identification of PRTS Inhibitors

Compounds to be tested are arrayed in the wells of a multi-well plate in varying concentrations along with an appropriate buffer and substrate, as described in the assays in Example XVII. PRTS activity is measured for each well and the ability of each compound to inhibit PRTS activity can be determined, as well as the dose-response kinetics. This assay could also be used to identify molecules which enhance PRTS activity.

In the alternative, phage display libraries can be used to screen for peptide PRTS inhibitors. Candidates are found among peptides which bind tightly to a protease. In this case, multi-well plate wells are coated with PRTS and incubated with a random peptide phage display library or a cyclic peptide library (Koivunen, E. et al. (1999) Nat. Biotechnol. 17:768-774). Unbound phage are washed away and selected phage amplified and rescreened for several more rounds. Candidates are tested for PRTS inhibitory activity using an assay described in Example XVII.

Various modifications and variations of the described methods and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with certain embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

Table 1

Incyte Project ID	Polypeptide SEQ ID NO:	Incyte Polypeptide ID	Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID
275791	1	275791CD1	22	275791CB1
1389845	2	1389845CD1	23	1389845CB1
1726609	3	1726609CD1	24	1726609CB1
4503848	4	4503848CD1	25	4503848CB1
5544089	5	5544089CD1	26	5544089CB1
7474081	6	7474081CD1	27	7474081CB1
5281209	7	5281209CD1	28	5281209CB1
2256251	8	2256251CD1	29	2256251CB1
7160544	9	7160544CD1	30	7160544CB1
7477386	10	7477386CD1	31	7477386CB1
7473089	11	7473089CD1	32	7473089CB1
7604035	12	7604035CD1	33	7604035CB1
3473847	13	3473847CD1	34	3473847CB1
3750004	14	3750004CD1	35	3750004CB1
4904126	15	4904126CD1	36	4904126CB1
71268415	16	71268415CD1	37	71268415CB1
7473301	17	7473301CD1	38	7473301CB1
7473308	18	7473308CD1	39	7473308CB1
7478021	19	7478021CD1	40	7478021CB1
4333459	20	4333459CD1	41	4333459CB1
6817347	21	6817347CD1	42	6817347CB1

Table 2

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability score	GenBank Homolog
1	275791CD1	g9971757	1.00E-49	ubiquitin-specific processing protease [Homo sapiens]
2	1389845CD1	g1143194	1.30E-46	prostasin [Homo sapiens]
3	1726609CD1	g10719660	0	RNPEP-like protein [Homo sapiens] (Horikawa, Y. et al. (2000) Nat. Genet. 26:163-175.)
4		g1754515	3.30E-96	aminopeptidase-B [Rattus norvegicus] (Prieto, I. et al. (1998) Horm. Metab. Res. 30:246-248.)
5	4503848CD1	g1783122	0	endopeptidase 24.16 type M1 [Sus scrofa]
6	5544089CD1	g5410230	5.20E-43	ubiquitin-specific protease 3 [Homo sapiens]
7	7474081CD1	g603903	2.90E-33	Trypsinogen [Gallus gallus]
8	5281209CD1	g11071729	0	putative dipeptidase [Homo sapiens]
9	2256251CD1	g219600	1.40E-88	dipeptidase precursor [Homo sapiens] (Sato, S. et al. (1993) Biochim. Biophys. Acta 1172:181-183.)
10	7160544CD1	g6103629	3.90E-166	transmembrane tryptase [Homo sapiens] (Wong, G.W. et al. (1999) J. Biol. Chem. 274:30784-30793.)
11	7477386CD1	g11095188	0	dipeptidyl peptidase 8 [Homo sapiens] (Abbott, C.A. et al. (2000) Eur. J. Biochem. 267:6140-6150.)
12	7473089CD1	g1753197	6.80E-64	dipeptidyl peptidase IV [Stenotrophomonas maltophilia] (Mentlein, R. (1999) Regul. Pept. 85:9-24; Kahne, T. Int. J. Mol. Med (1999) 4:3-15.)
		g1865716	0	procollagen I N-proteinase [Bos taurus] (Collige, A. et al. (1999) Am. J. Hum. Genet. 65:308-317.)
		g7768706	3.60E-255	metalloprotease with thrombospondin type 1 motifs [Homo sapiens] (Vazquez, F. et al. (1999) J. Biol. Chem. 274:23349-23357.)
	7604035CD1	g6164595	4.70E-68	Lacunin [Manduca sexta]

Table 2 (cont.)

Polypeptide SEQ ID NO:	Incyte Polypeptide ID	GenBank ID NO:	Probability score	GenBank Homolog
13	3473847CD1	g217172	9.20E-50	aqualysin precursor (aa 1 to 513) [Thermus aquaticus]
14	3750004CD1	g5923786	4.30E-51	zinc metalloprotease ADAMTS6 [Homo sapiens]
15	4904126CD1	g186286	3.90E-40	interleukin 1-beta convertase [Homo sapiens] (Cerretti, D.P. et al. (1992) Science 256:97-100.)
16	71268415CD1	g6651071	0	disintegrin and metalloprotease domain 19 [Homo sapiens] (Inoue, D. et al. (1998) J. Biol. Chem. 273:4180-4187.)
17	7473301CD1	g6002714	5.10E-94	membrane-type serine protease 1 [Homo sapiens] (Takeuchi, T. et al. (1999) Proc. Natl. Acad. Sci. USA 96:11054-11061.)
18	7473308CD1	g1552517	6.60E-77	trypsinogen E [Homo sapiens]
19	7478021CD1	g3211705	5.60E-189	matrix metalloprotease [Xenopus laevis] (Yang, M. (1997) J. Biol. Chem. 272:13527-13533.)
20	4333459CD1	g1754714	2.30E-67	Oviductin [Xenopus laevis] (Lindsay, L.L. et al. (1999) Biol. Reprod. 60:989-995.)
21	6817347CD1	g7673618	5.10E-283	ubiquitin specific protease [Mus musculus]

Table 3

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
1	275791CD1	232	T15 T17 S23 S43 S71 T90 S93 S100 S107 S111 T122 T174 S190 T10 S141 S190 T213 T227	N98 N99	Ubiquitin carboxyl-terminal hydrolase family 2 signature 2 Uch_2_2: Y142-Y160 Ubiquitin carboxyl-terminal hydrolase family 2 signature 2 UCH-2: L138-H203 Ubiquitin carboxyl-terminal hydrolase family 2 signature 2 BL00972: Y142-D166, K169-S190	MOTIFS HMMER-PFAM BLIMPS-BLOCKS
2	1389845CD1	365	S120 S187 S225 S253 S82 T31 T37 T42 Y283		TRYPSIN DM00018 A57014 45-284: I123-Q314 PROTEASE SERINE PRECURSOR SIGNAL HYDROLASE ZYMOGEN GLYCOPROTEIN FAMILY MULTIGENE FACTOR PD000046: I123-Q314 Serine proteases, trypsin family BL00134A: C148-C164 Kringle domain proteins BL00021: C148-F165, V231-G252 CHYMOTRYPSIN SERINE PROTEASE PR00722: G149-C164, G208-V222 V8 Serine proteases PR00839B: C148-F165 Serine proteases, trypsin family, active sites trypsin_his.prf: I140-P188 Trypsin: I123-Q314 Trypsin_His: L159-C164	BLAST_DOMO BLAST_PRODOR BLIMPS_BLOCKS BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRINTS PROFILES CAN HMMER_PFAM MOTIFS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
3	1726609CD1	416	S244 S283 S30 S370 S408 T389 T59 T78 T87	N203 N413 N57	do HYDROLASE; LEUKOTRIENE; A-4; ZINC; DM08707 P19602 7-609: M1-P354 AMINOPEPTIDASE HYDROLASE METALLOPROTEASE ZINC N GLYCOPROTEIN PROTEIN TRANSMEMBRANE SIGNAL ANCHOR MEMBRANE PD001134: R4-S177 Neutral zinc metalloproteinase family BL00142: D41-F51 MEMBRANE ALANYL DIPEPTIDASE PR00756: F14-L24, D41-T56, W60-Y72 signal_cleavage: M1-S34	BLAST_DOMO BLAST_PRODUM BLIMPS_BLOCKS BLIMPS_PRINTS SPScan
4	4503848CD1	714	S124 S140 S147 S179 S200 S206 S226 S333 S551 S556 S592 T114 T133 T244 T252 T270 T308 T318 T322 T376 T406 T432 T528 T585 T602 T69 Y175 Y249 Y505	N425 N485 N601	do ZINC; METALLOPEPTIDASE; NEUTRAL; OLIGO-PEPTIDASE DM01184 Q02038 36-702: A46-A713 HYDROLASE METALLOPROTEASE ZINC OLIGOPEPTIDASE PRECURSOR MITOCHONDRIAL ENDOPEPTIDASE MITOCHONDRION TRANSIT PEPTIDE PD002945: W60-N529 transmembrane domain: L14-M34 Peptidase family M3 Peptidase_M3: C98- L711 Neutral zinc metalloproteinase family BL00142: T504-H514 Zinc Protease: T504-M513 signal_cleavage: M1-G27	BLAST_PRODUM HMMER HMMER_PFBAM BLIMPS_BLOCKS MOTIFS SPScan

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
5	5544089CD1	367	S108 S161 S197 S203 S235 S266 S361 S49 T180 T263 T316 T331	N139 N142 N308	UBIQUITIN CARBOXYL-TERMINAL HYDROLASES FAMILY 2 DM00659 P40818 782-1103; L36-L328 Ubiquitin carboxyl-terminal hydrolase family BL00972: Y74-L83, V120-C134, Y274-N298, G301-K322 Ubiquitin carboxyl-terminal hydrolase family UCH-2: E270-Q332 Ubiquitin carboxyl-terminal hydrolase family Uch_2_2: Y274-Y292 signal_cleavage: M1-S16	BLAST_DOMO BLIMPS_BLOCKS HMMER_PFAM MOTIFS SPScan
6	7474081CD1	235	S134 S143 S159 S171 S226 T231	N90	TRYPSIN DM00018 S55065 26-244: A27-T231 Serine proteases, trypsin family signature BL00134: C40-C56, V215-I228 Type I fibronectin domain BL01253: C40-P53, I197-T231 Kringle domain proteins BL00021: S159-Q164, C40-Y57 CHYMOTRYPSIN SERINE PROTEASE PR00722A: V41-C56, A95-A109 Serine proteases, trypsin family, active site trypsin_his.prf: S35-T76 Trypsin: G42-V178, G216-I228 Leucine Zipper: L44-L65 signal_cleavage: M1-S19	BLAST_DOMO BLIMPS_BLOCKS BLIMPS_BLOCKS BLIMPS_BLOCKS BLIMPS_BLOCKS BLIMPS_PRINTS PROFILESAN HMMER_PFAM MOTIFS SPScan

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
7	5281209CD1	488	S13 T74 S186 S233 T363 T456 T4 T34 T125 S170 S172 T178 S249 T337 S387 S389 S419 T447	N119 N184 N243 N334	Renal dipeptidase proteins BL00869:P92-L247, E280-R412, S415-N457 DIPEPTIDASE MICROSOMAL PRECURSOR MDP HYDROLASE MICROSOME SIGNAL GPI-ANCHOR GLYCOPROTEIN ZINC PD005626:S143-E450 RENAL DIPEPTIDASE DM02775:T77-K410 Renal dipeptidase:V195-R217 Renal dipeptidase:A63-V475 Signal peptide:M1-A36 Signal cleavage:M1-A36	BLIMPS-BLOCKS BLAST-PRODOM BLAST-DOMO MOTIFS HMMER-PFAM HMMER SPSCAN
8	2256251CD1	346	S203 S210 S266 S45 S79 T131 T147 T216	N110	TRYPSIN DM00018 P15944 31-270: I63-I294 PROTEASE SERINE PRECURSOR SIGNAL HYDROLASE ZMOGEN GLYCOPROTEIN FAMILY MULTIGENE FACTOR PD000046: L156-I290, I63-F178, N288-F314, P274-P305 Serine proteases, trypsin family BL00134: C88-C104, D241-I264, P277-I290 Type I fibronectin domain BL01253: C88-A101, V158-E194, G240-C253, W259-H293 Kringle domain proteins BL00021: C88-F105, V169-G190, G249-I290 CHYMOTRYPSIN SERINE PROTEASE PR00722: G89-C104, G146-V160, G240-V252 transmembrane domain: P308-L328 trypsin: I63-I290 Trypsin_His L99-C104 Trypsin family serine protease active sites trypsin_his.prf: L80-H128 trypsin_ser.prf: L229-R273 signal_cleavage: M1-S45	BLAST_DOMO BLAST_PRODOM BLIMPS_BLOCKS BLIMPS_BLOCKS BLIMPS_BLOCKS BLIMPS_PRINTS HMMER HMMER_PFAM MOTIFS PROFILESKAN SPSCAN

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
9	7160544CD1	882	S115 S133 S293 S312 S412 S443 S479 S530 S587 S588 S723 S80 S850 T227 T234 T307 T326 T499 T52 T551 T594 T603 T615 T776 Y315 Y36 Y55 Y555 Y844		PROLYL ENDOPEPTIDASE FAMILY SERINE DM02461 P27487 192-765: F488-E870, G251-E370 DIPEPTIDYL IV HYDROLASE PROTEASE SERINE PEPTIDASE DIPEPTIDASE TRANSMEMBRANE GLYCOPROTEIN PROTEIN PD003048: L744-E870 DIPEPTIDYL IV HYDROLASE PROTEASE SERINE PEPTIDASE DIPEPTIDASE TRANSMEMBRANE GLYCOPROTEIN PROTEIN PD003086: Y423- V661, I212-T326 Prolyl endopeptidase family BL00708: G501-I513, Q714-L744 Dipeptidyl peptidase IV PF00930: I498- R508, F756-P783, R808-L828 PROLYL OLIGOPEPTIDASE SERINE PROTEASE PR00862: P647-F665, G737-R757 Prolyl oligopeptidase family Peptidase_S9: R672-L744 Dipeptidyl peptidase IV DPPIV_N_term: M88-N663	BLAST_DOMO BLAST_PRODUM BLAST_PRODUM BLIMPS_BLOCKS BLIMPS_PFAM BLIMPS_PRINTS HMMER_PFAM HMMER_PFAM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
10	7477386CD1	1189	S132 S169 S200 S32 S323 S350 S445 S480 S511 S626 S675 S699 S798 S1064 T247 T362 T521 T612 T718 T777 T946 T986 T1104 Y552	N109 N478 N944	do ZINC; METALLOPEPTIDASE; NEUTRAL; ATROLYSIN DM00368 Q05910 189-395:I261-P463 THROMBOSPONDIN TYPE 1 REPEAT DM00275 P07996 477-540: D555-C604 PROTEIN PROCOLLAGEN THROMBOSPONDIN MOTIFS NPROTEINASE C02B4.1 A DISINTEGRIN METALLOPROTEASE PD013511: L474-E549 PROTEIN PROCOLLAGEN THROMBOSPONDIN MOTIFS NPROTEINASE A DISINTEGRIN METALLOPROTEASE WITH ADAMTS1 PD011654: Q647-C716 PROCOLLAGEN C37C3.6 SERINE PROTEASE INHIBITOR PD007018: W854-Q974, W914-C1029, W558-K623 METALLOPROTEASE PRECURSOR HYDROLASE SIGNAL ZINC VENOM CELL PROTEIN TRANSMEMBRANE ADHESION PD000791:P2556-P463 Neutral zinc metalloproteinase BL00142: T398-N408 signal peptide: M1-A22 Reprolysin family propeptide Pep_M12B_propep: R120-V240 Reprolysin (M12B) family zinc metalloproteinase Reprolysin: I261-P463 Thrombospondin type 1 domain tsp_1: A973-C1024, S559-C609, Y852-C909, W914-C971 signal_cleavage: M1-G23	BLAST_DOMO BLAST_DOMO BLAST_PRODOM BLAST_PRODOM BLAST_PRODOM BLIMPS_BLOCKS HMMER HMMER_PFAM HMMER_PFAM HMMER_PFAM SPSCAN

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
11	7473089CD1	952	S19 S203 S207 S303 S346 S432 S492 S575 S578 S611 S666 S682 S708 S745 S919 T171 T288 T317 T325 T337 T359 T471 T594 T687 T765	N141 N591 N623 N680	do ZINC; METALLOPEPTIDASE; NEUTRAL; ATROLYSIN DM00368 JC2550 1-201:R218-P427 PROTEIN PROCOLLAGEN THROMBOSPONDIN MOTIFS NPROTEINASE A DISINTEGRIN METALLOPROTEASE WITH ADAMTS1 PD014161: K684-E804 PROTEIN PROCOLLAGEN THROMBOSPONDIN MOTIFS NPROTEINASE A DISINTEGRIN METALLOPROTEASE WITH ADAMTS1 PD011654: V610-C683 METALLOPROTEASE PRECURSOR HYDROLASE SIGNAL ZINC VENOM CELL PROTEIN TRANSMEMBRANE ADHESION PD000791: V214-P427 PROTEIN PROCOLLAGEN THROMBOSPONDIN MOTIFS NPROTEINASE C02B4.1 A DISINTEGRIN METALLOPROTEASE PD013511: L437-V505 Neutral zinc metalloproteinase BL00142: T358-N368 signal peptide: M1-G18 Reprolysin family propeptide Pep_M12B_propep: H67-N181 Reprolysin (M12B) family zinc metalloproteinase Reprolysin: R218-P427 Thrombospondin type 1 domain tsp_1: A520-C570, W845-C896, W899-C952 Zinc_Protease: T358-F367 SpScan signal_cleavage: M1-G17	BLAST_DOMO BLAST_PRODUM BLAST_PRODUM BLAST_PRODUM BLIMPS_BLOCKS HMIMER HMIMER_PFAM HMIMER_PFAM HMIMER_PFAM MOTIFS SPSCAN

Table 3 (cont.)

SEQ ID NO:	Incyte polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
12	7604035CD1	898	S187 S188 S258 S268 S285 S415 S467 S547 S696 S796 S819 S851 S892 T106 T198 T35 T434 T483 T492 T5	N3 N490 N773	PROCOLLAGEN C37C3.6 SERINE PROTEASE INHIBITOR ALTERNATIVE PD007018: Y726-C841, W786-A874, Y667-C778, W50-Q72, S368-Q383 PROTEIN PROCOLLAGEN THROMBOSPONDIN MOTIFS NPROTEINASE A DISINTEGRIN METALLOPROTEASE WITH ADAMTS1 PD011654: Q416-C484 PROTEIN PROCOLLAGEN THROMBOSPONDIN MOTIFS NPROTEINASE A DISINTEGRIN METALLOPROTEASE WITH ADAMTS1 PD014161: R485-I599 signal_peptide: M1-D24 Thrombospondin type 1 domain tsp_1: G48-R87, W727-C783, E787-C841 signal_cleavage: M1-D24	BLAST_PRODOM BLAST_PRODOM BLAST_PRODOM BLAST_PRODOM HMMER HMMER_PFAM SPSCAN
13	3473847CD1	631	S117 S160 S174 S185 S188 S268 S28 S30 S358 S431 S503 S605 T142 T33 T346 T512 T606	N472	Subtilase family Peptidase_S8: S86-N364 SERINE PROTEASES, SUBTILASE FAMILY, HISTIDINE DM00108 P80146 150-377: G116-T346 Serine proteases, subtilase family BL00136: L123-I135, D163-G175, G323-G333 SUBTILISIN SERINE PROTEASE FAMILY PR00723: G116-I135, K161-S174, S322-M338 Serine proteases, subtilase family, active site subtilase ser.pr.f: A302-Q352	HMMER_PFAM BLAST_DOMO BLIMPS_BLOCKS BLIMPS_PRINTS PROFILES CAN

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
14	3750004CD1	470	S454 S51 S54 T104 T276 T386 T464	N182 N203	Thrombospondin type 1 domain tsp_1: T34-C81 PROTEIN PROCOLLAGEN THROMBOSPONDIN MOTIFS NPROTEINASE A DISINTEGRIN METALLOPROTEASE WITH ADAMTS1 PD011654: Q119-C185 signal_peptide: M1-G29 signal_cleavage: M1-G24	HMMER_PFAM BLAST_PRODOR
15	4904126CD1	110	S16 S36 T100 T49 N47		Caspase recruitment domain CARD: A2-A91 INTERLEUKIN-1 BETA CONVERTING ENZYME FAMILY HISTIDINE DM07463 P29466 1-122: M1-S110	HMMER SPScan HMMER_PFAM BLAST_DOMO

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
16	71268415CD1	879	S132 S14 S208 S288 S571 S711 S747 S754 S755 S827 T106 T118 T29 T30 T373 T412 T42 T428 T444 T55 T688 Y167 Y39	N368 N371 N569 N68	Reprolysin family propeptide Pep_M12B_propep: R8-K119 Reprolysin (M12B) family zinc metalloprotease Reprolysin: K134-P332 Disintegrin: E349-Q424 do-ZINC; METALLOPEPTIDASE; NEUTRAL; ATROLYSIN; DM00368 S60257 204-414: K126-D333 do ZINC; REGULATED; EPIDIDYMAL; NEUTRAL; DM00591 S60257 492-628: F410-L549 MELTRIN, BETA METALLOPROTEASE DISINTEGRIN BETA INTEGRIN PROTEASE METALLOPROTEASE PD105322: P620-G812 METALLOPROTEASE PRECURSOR HYDROLASE SIGNAL ZINC VENOM CELL PROTEIN TRANSMEMBRANE ADHESION PD000791: K134-P332 MELTRIN, BETA METALLOPROTEASE DISINTEGRIN MELTRIN BETA INTEGRIN PROTEASE METALLOPROTEASE PD171676: K495-C567 CELL ADHESION PLATELET BLOOD COAGULATION VENOM DISINTEGRIN METALLOPROTEASE PRECURSOR SIGNAL PD000664: E349-Y423 Neutral zinc metalloprotease BL00142: T266-G276 DISINTEGRIN SIGNATURE PR00289: C380-R399, E409-N421 NEPRILYSIN METALLOPROTEASE PR00786C: N259-F275	HMMER_PFAM HMMER_PFAM HMMER_PFAM BLAST_DOMO BLAST_DOMO BLAST_PRODROM BLAST_PRODROM BLAST_PRODROM BLAST_PRODROM BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRINTS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
17	7473301CD1	850	S100 S275 S295 S358 S429 S448 S470 S474 S495 S536 S596 S64 S787 S802 S807 T117 T250 T312 T348 T382 T404 T426 T570 T714 T777	N19 N210 N422 N486 N533 N559 N568	Disintegrins signature disintegrins.prf: E360-P419 Neutral zinc metalloproteinases, zinc-binding region signature zinc_protease.prf: S249-G301 transmembrane domain: V624-Y645 Zn binding region Zinc_Protease: T266-F275 TRYPSIN FAMILY SERINE PROTEASE trypsin: I613-I842 Low-density lipoprotein receptor domain ldl_recept_a: Q489-S527, P530-Q562, I564-C603 TRYPSIN DM00018 P98072 800-1033: R612-V846 PROTEASE SERINE PRECURSOR SIGNAL HYDROLASE ZYMOGEN GLYCOPROTEIN FAMILY MULTIGENE FACTOR PD000046: Q675-I842, I613-G809 Serine proteases, trypsin family BL00134: C638-C654, D791-T814, P829-I842 Type I fibronectin domain BL01253: C638-A651, R790-C803, W811-Y845 Kringlet domain proteins BL00021: I722-G743, L801-I842, C638-F655 LOW DENSITY LIPOPROTEIN RECEPTOR DOMAIN PR00261: G501-E522 CHYMOTRYPSIN SERINE PROTEASE PR00722: G639-C654, T697-W711, R790-S802	PROFILES SCAN PROFILES SCAN HMMER MOTIFS HMMER_PFAM HMMER_PFAM BLAST_DOMO BLAST_PRODOM BLIMPS_BLOCKS BLIMPS_BLOCKS BLIMPS_BLOCKS BLIMPS_PRINTS BLIMPS_PRINTS

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Trypsin family serine protease active sites trypsin_his.prf: L630-K679 trypsin_ser.prf: I776-R825 transmembrane domain: I77-L95 Trypsin family serine protease active sites Trypsin_His L649-C654 Trypsin_Ser D791-S802	PROFILERSCAN HMMER MOTIFS
18	7473308CD1	254	S136 S14 S153 S195 S227 T230 T249		TRYPSIN FAMILY SERINE PROTEASE trypsin: I21-Q183 CHYMOTRYPSIN SERINE PROTEASE FAMILY PR00722B: T89-A103 TRYPSIN DM00018 P07478 24-242: I21-Q183 PROTEASE SERINE PRECURSOR SIGNAL HYDROLASE ZYMOGEN GLYCOPROTEIN FAMILY MULTIGENE FACTOR PD000046: G23-Q183	HMMER_PFAM BLIMPS_PRINTS BLAST_DOMO BLAST_PRODOM

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
19	7478021CD1	568	S142 S145 S153 S172 S177 S190 S244 S316 S34 S420 S448 S552 T209 T22 T293 T334 T401 T427 T489 T79 Y509	N371	Matrixin Peptidase_M10: F56-T266 Hemopexin domain: F332-T390, I393-S448, L450-Q498, I505-K548 MATRIXINS CYSTEINE SWITCH DM00558 P22757 100-337: A184-T334, P76-P124 MATRIXINS CYSTEINE SWITCH DM00558 P08254 29-274: Q158-T334, L85-M122 MATRIX METALLOPROTEINASE PD168921: S327-N392 MATRIX METALLOPROTEINASE PD169970: A494-M568 MATRIX PRECURSOR METALLOPROTEINASE HYDROLASE ZINC ZYMOGEN CALCIUM COLLAGEN DEGRADATION SIGNAL PD000673: F171-T266, P73-M122 Matrixins cysteine switch BL00546: F92-D121, V224-P267, G273-Y304, L313-G326, F443-Y455, F409-E428 Hemopexin domain protein BL00024: M112-M122, G273-Y304, L313-G326, F443-Y455, Y408-D419 MATRIXIN SIGNATURE PRO0138: M112-P125, E198-F213, V224-W252, V279-Y304, L313-G326 Matrixins cysteine switch cysteine_switch.prf: A95-M204 Neutral zinc metalloproteinases, zinc-binding region signature zinc_protease.prf: D256-E312	HMMER_PFAM HMMER_PFAM BLAST_DOMO BLAST_DOMO BLAST_PRODUM BLAST_PRODUM BLAST_PRODUM BLIMPS_BLOCKS BLIMPS_BLOCKS BLIMPS_PRINTS PROFILES SCAN PROFILES SCAN

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
					Hemopexin domain signature hemopexin.prf: F409-R477 signal_peptide: M1-P21 Zn binding region Zinc_Protease: V279-L288 signal_cleavage: M1-P24	PROFILESSCAN HMMER MOTIFS SPScan
20	4333459CD1	306	S117 S138 S2 S223 S60 S72 T110 T139 T207 T217	N108	TRYPSIN FAMILY SERINE PROTEASE trypsin: I56-I298 TRYPSIN DM00018 Q05319 543-784: I56-I302 PROTEASE SERINE PRECURSOR SIGNAL HYDROLASE ZYMOGEN GLYCOPROTEIN FAMILY MULTIGENE FACTOR PD000046: S117-I298, I56-G192 Serine proteases, trypsin family BL00134: C81-C97, D238-G261, P285-I298 Type I fibronectin domain BL01253: C81-A94, G154-E190, R237-C250 Kringle domain proteins BL00021: C81-I98, I165-G186, S247-F288 CHYMOTRYPSIN SERINE PROTEASE PR00722: G82-C97, P142-F156, R237-M249 Trypsin family serine protease active sites trypsin_his.prf: L73-G122 trypsin_ser.prf: K225-R271 Trypsin family serine protease active sites Trypsin_His: I92-C97 Trypsin_Ser: D238-M249 signal_cleavage: M1-S26	BLAST_DOMO BLAST_PRODOR BLIMPS_BLOCKS BLIMPS_BLOCKS BLIMPS_BLOCKS BLIMPS_PRINTS PROFILESSCAN MOTIFS SPScan

Table 3 (cont.)

SEQ ID NO:	Incyte Polypeptide ID	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequences, Domains and Motifs	Analytical Methods and Databases
21	6817347CD1	953	S102 S114 S150 S172 S369 S429 S47 S623 S794 S804 S808 S831 S856 S919 S942 T289 T42 T455 T488 T544 T567 T568 T585 T59 T736 T777 T786 T839 Y929	N95	Ubiquitin carboxyl-terminal hydrolase family 1 UCH-1: R593-D624 Ubiquitin carboxyl-terminal hydrolase family 2 UCH-2: N875-K935 UBIQUITIN CARBOXYL-TERMINAL HYDROLASES FAMILY 2 DM00659 P40818 782-1103: T777-L931, L598-H709, I713-T753, V101-L128 PROTEASE UBIQUITIN HYDROLASE UBIQUITIN SPECIFIC ENZYME DEUBIQUITINATING C-TERMINAL THIOLESTERASE PROCESSING CONJUGATION PD017412: T777-E859 Ubiquitin carboxyl-terminal hydrolase family 2 BL00972: G594-L611, Y675-L684, I714-C728, K878-H902, K904-D925 Ubiquitin carboxyl-terminal hydrolase family 2 signature 1 Uch_2_1: G594-Q609 Ubiquitin carboxyl-terminal hydrolase family 2 signature 2 Uch_2_2: Y879-Y896	HMMER_PFAM HMMER_PFAM BLAST_DOMO BLAST_PRODOR BLIMPS_BLOCKS MOTIFS MOTIFS

Table 4

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
22	275791CB1	2204	1168-1197, 1503-1522, 1-281, 1716-1738	6456514H1 (COLNDIC01)	890	1510
				7246467T8 (PROSTM01)	692	1390
				4943009F8 (BRAIFEN05)	1319	1877
				55047202J1	1	811
				6053385H1 (BRABDIR03)	1636	2204
				FL1389845_00001	6	2036
23	1389845CB1	2036	1-392, 1468-1491, 1334-1400, 1974-2036	1389845H1 (EOSINOT01)	1	244
24	1726609CB1	2185	1-44, 1804- 2185	71762189V1	1	662
				5426388F9 (PROSTM07)	1370	1992
				71053940V1	744	1373
				71041539V1	1954	2185
				5968441H1 (BRAZNOT01)	1326	1824
				6756865J1 (SINTFER02)	642	1316
				2053131H1 (BEPINOT01)	2885	3136
				6440674H1 (BRAENOT02)	2576	3095
25	4503848CB1	3486	1-1330	g5745066	1831	2254
				7191212H2 (BRATDIC01)	2295	2873
				5960039H1 (BRATNOT05)	1229	1797
				GBI.g7710158_edit	1	2015
				60200050D1	825	1146
				5969176H1 (BRAZNOT01)	1677	2104
				5649471H1 (BRAITUT23)	3157	3486
				2232143F6 (PROSNOT16)	2235	2670
				3022114H1 (PROSDIN01)	3116	3402
				60220456D1	1085	1462

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
26	5544089CB1	2847	1260-1631, 2532-2847, 408-914	55051688J1	810	1767
				2344450F6 (TESTTUT02)	2195	2847
				7658834H1 (OVARNOE02)	2130	2642
				71763578V1	1562	2266
				6576463H1 (COLHTUS02)	1079	1838
27	7474081CB1	890	1-21	55051680J1, comp g2103202	1	958
28	5281209CB1	1577	1-629	g2142177	1	493
				FL5281209_g7712102_000	397	890
				004_g436191	1	1467
29	2256251CB1	1958	1-399, 896-935	g3644494	1155	1577
				3142983R6 (HNT2AZS07)	1045	1576
				3220504T6 (COLNNON03)	1611	1958
				g4264312	400	848
				FL2256251_g7708357_000	910	1830
30	7160544CB1	3106	1-540, 1166-1428	002_g6103629		
				2256251R6 (OVARTUT01)	408	1003
				6471337H1 (PLACFEB01)	1654	2316
				6854305H1 (BRAIFEN08)	895	1561
				4443368H1 (SINDNOT01)	1332	1585
				6894004J1 (BRAITDR03)	470	1077
				7655990H1 (UTREDME06)	324	822
				7745974H1 (ADRETUE04)	2378	3052
				7160544H1 (HNT2TXC01)	1	427
				70490289V1	2636	3106
				70748463V1	2269	2891
				7745974J1 (ADRETUE04)	1566	2153

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
31	7477386CB1	3567	1-971, 1953-2846, 3243-3567	GBI:g6682143_000029_ed it.20231-20345 GBI:g6682143_000023.co mp_edit.11365-11445 GBI:g6682143_000027_ed it.14110-14265 GBI:g6682143_000029_ed it.35032-35202 GBI:g6682143_000029_ed it.13651-13803 GBI:g6682143_000019_ed it.3461-3655 GBI:g6682143_000029_ed it.41513-41644 GBI:g6682143_000029_ed it.43912-44404 GBI:g6682143_000029_ed it.12846-12930 GBI:g6682143_000029_ed it.15804-15912 GBI:g6682143_000023.co mp_edit.9253-9693 GBI:g6682143_000029_ed it.27621-27746 GBI:g6682143_000029_ed it.18722-18853 GBI:g6682143_000029_ed it.17438-17581 GBI:g6682143_000029_ed it.35651-35783	1495 1 523 2272 958 679 2944 3076 874 1111 82 2068 1363 1219 2608	1608 81 678 2436 1110 873 3075 3567 957 1218 522 2193 1494 1362 2739

Table 4

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
22	275791CB1	2204	1168-1197, 1503-1522, 1-281, 1716-1738	6456514H1 (COLNDIC01)	890	1510
				7246467T8 (PROSTMY01)	692	1390
				4943009F8 (BRAIFEN05)	1319	1877
				55047202J1	1	811
				6053385H1 (BRABDIR03)	1636	2204
23	1389845CB1	2036	1-392, 1468-1491, 1334-1400, 1974-2036	FL1389845_00001	6	2036
				1389845H1 (EOSINOT01)	1	244
24	1726609CB1	2185	1-44, 1804- 2185	71762189V1	1	662
				5426388F9 (PROSTMT07)	1370	1992
				71053940V1	744	1373
25	4503848CB1	3486	1-1330	71041539V1	1954	2185
				5968441H1 (BRAZNOT01)	1326	1824
				6756865J1 (SINTFER02)	642	1316
				2053131H1 (BEPINOT01)	2885	3136
				6440674H1 (BRAENOT02)	2576	3095
				95745066	1831	2254
				7191212H2 (BRATDIC01)	2295	2873
				5960039H1 (BRATNOT05)	1229	1797
				GBI.g7710158_edit	1	2015
				602000501 ¹⁰	825	1146
				5969176H1 (BRAZNOT01)	1677	2104
				5649471H1 (BRAITUT23)	3157	3486
				2232147F5 (EROSNOT16)	2235	2670
				3022114.1 (PROSDIN01)	3116	3402
				60220456D1	1085	1462

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
26	5544089CB1	2847	1260-1631, 2532-2847, 408-914	55051688J1	810	1767
				23444450F6 (TESTTUT02)	2195	2847
				7658834H1 (OVARNOE02)	2130	2642
				71763578V1	1562	2266
				6576463H1 (COLHTUS02)	1079	1838
27	7474081CB1	890	1-21	55051680J1.comp	1	958
				g2103202	1	493
				g2142177	397	890
28	5281209CB1	1577	1-629	FL5281209_g7712102_000	1	1467
				004_g436191		
				g3644494	1155	1577
				3142983R6 (HNT2AZS07)	1045	1576
				3220504T6 (COLNNON03)	1611	1958
29	2256251CB1	1958	1-399, 896-935	g4264312	400	848
				FL2256251_g7708357_000	910	1830
				002_g6103629		
				2256251R6 (OVARTUT01)	408	1003
				6471337H1 (PLACFEB01)	1654	2316
30	7160544CB1	3106	1-540, 1166-1428	6854305H1 (BRAIFEN08)	895	1561
				4443368H1 (SINDNOT01)	1332	1585
				6894004J1 (BRALTDR03)	470	1077
				7655990H1 (UTREDME06)	324	822
				7745974H1 (ADRETUE04)	2378	3052
				7160544H1 (HNT2FXC01)	1	427
				70490289V1	2636	3106
				70748463V1	2269	2891
				7745974J1 (ADRETUE04)	1566	2153

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
31	7477386CB1	3567	1-971, 1953-2846, 3243-3567	GBI:g6682143_000029_ed it.20231-20345	1495	1608
				GBI:g6682143_000023.co mp_edit.11365-11445	1	81
				GBI:g6682143_000027_ed it.14110-14265	523	678
				GBI:g6682143_000029_ed it.35032-35202	2272	2436
				GBI:g6682143_000029_ed it.13651-13803	958	1110
				GBI:g6682143_000019_ed it.3461-3655	679	873
				GBI:g6682143_000029_ed it.41513-41644	2944	3075
				GBI:g6682143_000029_ed it.43912-44404	3076	3567
				GBI:g6682143_000029_ed it.12846-12930	874	957
				GBI:g6682143_000029_ed it.15804-15912	1111	1218
				GBI:g6682143_000023.co mp_edit.9253-9693	82	522
				GBI:g6682143_000029_ed it.27621-27746	2068	2193
				GBI:g6682143_000029_ed it.18722-18853	1363	1494
				GBI:g6682143_000029_ed it.17438-17581	1219	1362
				GBI:g6682143_000029_ed it.35651-35783	2608	2739

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
32	7473089CB1	2930	1-632, 1082-1138, 2453-2555, 1373-1615, 1716-1740	GBI:g6682143_000029_ed it.27099-27237	1759	1932
				GBI:g6682143_000029_ed it_24540-24713	1609	1758
				GBI:g6682143_000029_ed it.37355-37558	2740	2943
				GBI:g7387384_000011.co mp_edit.13491-13892	2529	2930
				GBI:g7387384_000010_ed it.2924-3211	1335	1619
				GBI:g7387384_000010_ed it.13479-13850	2157	2528
				GBI:g7387384_000010_ed it.11350-11535	1794	1979
				7988641H1 (UTRSTUC01)	1064	1587
				GBI:g7387384_000010_ed it.9694-9867	1620	1793
				GBI:g7387384_000012.co mp_edit_9639-10595	75	1031
				GBI:g7387384_000010_ed it.1917-2074	1032	1163
				GBI:g7387384_000010_ed it.2514-2684	1164	1334
				7631548J1 (BRAFTUE03)	21	619
				GBI:g7387384_000010_ed it.11639-11815	1980	2156
				GBI:g7387384_edit	1	2930

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
33	7604035CB1	4230	4185-4230, 894-2774	6254235H1 (LUNPTUT02)	3308	3897
				6213818H1 (MUSCDIT06)	3900	4230
				6314348H1 (NERDTDN03)	3426	3994
				7195502H1 (LUNGFER04)	2758	3376
				6800634J1 (COLENOT03)	2678	3323
				8113675H1 (OSTEUNC01)	1661	2049
				6804059H1 (COLENOT03)	478	1050
				7750274H1 (HEAONOE01)	1995	2503
				3843227F6 (DENDNOT01)	2094	2707
				7632961H1 (BLADTUE01)	1418	2024
				55097977J1	688	1535
				7716357J1 (SINTFEE02)	1	678
				71906145V1	1340	2118
				7101935F8 (BRAWTDR02)	166	760
				70857826V1	2757	3441
34	3473847CB1	3699	1-2631	70855756V1	2650	3239
				820867R1 (KERANOT02)	2166	2732
				8055446J1 (ESOGTUE01)	579	1013
				70857738V1	3156	3699
				70858612V1	1998	2671
				GNN.g7208751_000002_00	555	1850
				2.edit		
				7101935R8 (BRAWTDR02)	1	473

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment (s)	Sequence Fragments	5' Position	3' Position
35	3750004CB1	2410	1-264, 2116-2410, 1057-1167, 1590-1649	g7712021_edit 7680089J1 (BRAFTUE01) 6804411H1 (COLENOR03) 71909368V1 g1187194 g2241985 6314962H1 (NERDTDN03) 6823371J1 (SINTNOR01) 7655009J1 (UTREDME06) g1272147 71620969V1 7715927J1 (SINTFEE02) 7372052H2 (BRAIFEE04) g6651070_CD 7723192J2 (THYRDIE01) GBI:g7709257_000011.ed it 8037549H1 (SMCRUNE01) 7720289J1 (THYRDIE01) 8037549J1 (SMCRUNE01)	1 1327 1088 536 1655 706 973 65 1407 1754 1 590 2044 102 905 1 206 1596 1456	246 1911 1618 968 2127 1144 1135 855 1990 2410 549 1340 2514 2755 1500 139 819 2263 2120
36	4904126CB1	549				
37	71268415CB1	2755	1-1097, 2326-2755			

Table 4 (cont.)

Polynucleotide SEQ ID NO:	Incyte Polynucleotide ID	Sequence Length	Selected Fragment(s)	Sequence Fragments	5' Position	3' Position
38	7473301CB1	2553	1-2394	GBL.g7272157_000017.ed it 71704195V1 5544473H1 (TESTNOC01) GNN.g7272157_000017_00 2.edit 5544473T8 (TESTNOC01) 71703469V1 GNN.g8571511_000004_00 2.edit GNN.g6624046_000008_00 4 GNN.g1552511_035 g8176728.edit g7684439.edit g7684439.edit_2 71571956V1 5634861R8 (PLACFER01) 71571988V1 71573159V1 55022864H1 55022792H2 55022814H1 55022795J2 GNN.g7417337_004.edit	2001 1713 622 1688 2246 1163 981 1 1 979 1 1084 704 1 256 247 2314 1392 2080 2044 1	2553 2016 680 2382 2550 1746 1468 1111 1041 1083 978 1707 1262 266 937 928 3067 2091 2886 2726 3067
39	7473308CB1	1041	826-1041, 1-299		1	1111
40	7478021CB1	1707	1-1188		1	1041
41	4333459CB1	1262	1-1262		1084 704 1 256 247 2314 1392 2080 2044 1	1707 1262 266 937 928 3067 2091 2886 2726 3067
42	6817347CB1	3067	1-2270		1	3067

Table 5

Polynucleotide SEQ ID NO:	Incyte Project ID	Representative Library
22	275791CB1	TESTNOT03
23	1389845CB1	EOSITXT01
24	1726609CB1	BRAITUT02
25	4503848CB1	PROSNOT16
26	5544089CB1	BRAIFEC01
28	5281209CB1	HNT2AZS07
29	2256251CB1	OVARTUT01
30	7160544CB1	BRAFNOT02
32	7473089CB1	UTRSTUC01
33	7604035CB1	PLACNOR01
34	3473847CB1	KERANOT02
35	3750004CB1	BRAFTUE01
36	4904126CB1	TLYMNOT08
37	71268415CB1	THYRDIE01
38	7473301CB1	TESTNOC01
41	4333459CB1	KIDCTMT01
42	6817347CB1	ADRETUR01

Table 6

Library	Vector	Library Description
ADRETUR01	PCDNA2.1	This random primed library was constructed using RNA isolated from left upper pole, adrenal gland tumor tissue removed from a 52-year-old Caucasian male during nephroureterectomy and local destruction of renal lesion. Pathology indicated grade 3 adrenal cortical carcinoma forming a mass that infiltrated almost the whole adrenal parenchyma and extended to adjacent adipose tissue. A metastatic tumor nodule was identified in the hilar region. The renal vein was infiltrated by tumor and the neoplastic process was present at the resection margin of the renal vein. Fragments of adrenal cortical carcinoma and thrombus were found in the inferior vena cava. Patient history included abnormal weight loss. Family history included skin cancer, type I diabetes, and neurotic depression.
BRAFNOT02	pINCY	Library was constructed using RNA isolated from superior frontal cortex tissue removed from a 35-year-old Caucasian male who died from cardiac failure. Pathology indicated moderate leptomeningeal fibrosis and multiple microinfarctions of the cerebral neocortex. Microscopically, the cerebral hemisphere revealed moderate fibrosis of the leptomeninges with focal calcifications. There was evidence of shrunken and slightly eosinophilic pyramidal neurons throughout the cerebral hemispheres. In addition, scattered throughout the cerebral cortex, there were multiple small microscopic areas of cavitation with surrounding gliosis. Patient history included dilated cardiomyopathy, congestive heart failure, cardiomegaly, and an enlarged spleen and liver.
BRAFTUE01	PCDNA2.1	This 5' biased random primed library was constructed using RNA isolated from brain tumor tissue removed from the frontal lobe of a 58-year-old Caucasian male during excision of a cerebral meningeal lesion. Pathology indicated a grade 2 metastatic hypernephroma. The patient presented with migraine headache. The patient developed a cerebral hemorrhage and pulmonary edema, and died during this hospitalization. Patient history included a grade 2 renal cell carcinoma, insomnia, and chronic airway obstruction. Previous surgeries included a nephroureterectomy. Patient medications included Decadron and Dilantin. Family history included a malignant neoplasm of the kidney in the father.
BRAIFEC01	pINCY	This large size-fractionated library was constructed using RNA isolated from brain tissue removed from a Caucasian male fetus who was stillborn with a hypoplastic left heart at 23 weeks' gestation.

Table 6 (cont.)

Library	Vector	Library Description
BRAITUT02	PSPORT1	Library was constructed using RNA isolated from brain tumor tissue removed from the frontal lobe of a 58-year-old Caucasian male during excision of a cerebral meningial lesion. Pathology indicated a grade 2 metastatic hypernephroma. Patient history included a grade 2 renal cell carcinoma, insomnia, and chronic airway obstruction. Family history included a malignant neoplasm of the kidney.
EOSITXT01	pINCY	Library was constructed using RNA isolated from eosinophils stimulated with IL-5.
HNT2AZS07	PSPORT1	This subtracted library was constructed from RNA isolated from an hNT2 cell line (derived from a human teratocarcinoma that exhibited properties characteristic of a committed neuronal precursor) treated for three days with 0.35 micromolar AZ. The hybridization probe for subtraction was derived from a similarly constructed library from untreated hNT2 cells. 3.08M clones from the AZ-treated library were subjected to three rounds of subtractive hybridization with 3.04M clones from the untreated library. Subtractive hybridization conditions were based on the methodologies of Swaroop et al. (NAR (1991) 19:1954) and Bonaldo et al. (Genome Research (1996) 6:791).
KERANOT02	PSPORT1	Library was constructed using RNA isolated from epidermal breast keratinocytes (NHEK). NHEK (Clontech #CC-2501) is human breast keratinocyte cell line derived from a 30-year-old black female during breast-reduction surgery.
KIDCTMT01	pINCY	Library was constructed using RNA isolated from kidney cortex tissue removed from a 65-year-old male during nephroureterectomy. Pathology for the associated tumor tissue indicated grade 3 renal cell carcinoma within the mid-portion of the kidney and the renal capsule.
OVARTUT01	PSPORT1	Library was constructed using RNA isolated from ovarian tumor tissue removed from a 43-year-old Caucasian female during removal of the fallopian tubes and ovaries. Pathology indicated grade 2 mucinous cystadenocarcinoma involving the entire left ovary. Patient history included mitral valve disorder, pneumonia, and viral hepatitis. Family history included atherosclerotic coronary artery disease, pancreatic cancer, stress reaction, cerebrovascular disease, breast cancer, and uterine cancer.

Table 6 (cont.)

Library	Vector	Library Description
PLACNOR01	PCDNA2.1	This random primed library was constructed using pooled cDNA from two different donors. cDNA was generated using mRNA isolated from placental tissue removed from a Caucasian fetus (donor A), who died after 16 weeks' gestation from fetal demise and hydrocephalus and from placental tissue removed from a Caucasian male fetus (donor B), who died after 18 weeks' gestation from fetal demise. Patient history for donor A included umbilical cord wrapped around the head (3 times) and the shoulders (1 time). Serology was positive for anti-CMV and remaining serologies were negative. Family history included multiple pregnancies and live births, and an abortion in the mother. Serology was negative for donor B.
PROSNOT16	pINCY	Library was constructed using RNA isolated from diseased prostate tissue removed from a 68-year-old Caucasian male during a radical prostatectomy. Pathology indicated adenofibromatous hyperplasia. Pathology for the associated tumor tissue elevated prostate specific antigen (PSA). The patient presented with type II diabetes. Family history included benign hypertension, acute myocardial infarction, hyperlipidemia, and arteriosclerotic coronary artery disease.
TESTNOC01	PBLUESCRIPT	This large size fractionated library was constructed using RNA isolated from testicular tissue removed from a pool of eleven, 10 to 61-year-old Caucasian males.
TESTNOT03	PBLUESCRIPT	Library was constructed using RNA isolated from testicular tissue removed from a 37-year-old Caucasian male, who died from liver disease. Patient history included cirrhosis, jaundice, and liver failure.
THYRDIE01	PCDNA2.1	This 5' biased random primed library was constructed using RNA isolated from diseased thyroid tissue removed from a 22-year-old Caucasian female during closed thyroid biopsy, partial thyroidectomy, and regional lymph node excision. Pathology indicated adenomatous hyperplasia. The patient presented with malignant neoplasm of the thyroid. Patient history included normal delivery, alcohol abuse, and tobacco abuse. Previous surgeries included myringotomy. Patient medications included an unspecified type of birth control pills. Family history included hyperlipidemia and depressive disorder in the mother; and benign hypertension, congestive heart failure, and chronic leukemia in the grandparent(s).

Table 6 (cont.)

Library	Vector	Library Description
TLVMNOT08	pINCY	The library was constructed using RNA isolated from anergic/allogenic T-lymphocyte tissue removed from an adult (40-50-year-old) Caucasian male. The cells were incubated for 3 days in the presence of 1 microgram/ml OKT3 mAb and 5% human serum.
UTRSTUC01	PSPORT1	This large size fractionated library was constructed using pooled cDNA from two donors. cDNA was generated using mRNA isolated from uterus tumor tissue removed from a 37-year-old Black female (donor A) during myomectomy, dilation and curettage, right fimbrial region biopsy, and incidental appendectomy; and from endometrial tumor tissue removed from a 49-year-old Caucasian female (donor B) during vaginal hysterectomy and bilateral salpingo-oophorectomy. For donor A, pathology indicated multiple uterine leiomyomata. A fimbrial cyst was identified. The endometrium was in secretory phase with hormonal effect. The patient presented with deficiency anemia, an umbilical hernia, and premenopausal menorrhagia. Patient history included premenopausal menorrhagia and sarcoidosis of the lung. Previous surgeries included hysteroscopy, dilation and curettage, and endoscopic lung biopsy. Patient medications included Chromagen and Claritin. For donor B, pathology indicated grade 3 adenocarcinoma forming a mass within the uterine fundus and involving the anterior uterine wall, as well as focally involving an adjacent endometrial polyp. The tumor invaded to a maximum depth of 7mm (uninvolved wall thickness, 2.2cm). The adjacent endometrium was inactive. Paraffin section immunostains for estrogen receptors and progesterone receptors were positive. Patient history included malignant breast neoplasm. Previous surgeries included unilateral extended simple mastectomy and bilateral tubal destruction. Patient medications included Megace and CAF (Cyclophosphamide, Adriamycin, Fluorouracil).

Table 7

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25:3389-3402.	ESTs: Probability value= 1.0E-8 or less Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad. Sci. USA 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183:63-98; and Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value=1.0E-6 Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less Full Length sequences: fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) Nucleic Acids Res. 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37:417-424.	Probability value= 1.0E-3 or less
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) J. Mol. Biol. 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322; Durbin, R. et al. (1998) Our World View, in a Nutshell, Cambridge Univ. Press, pp. 1-350.	PFAM hits: Probability value= 1.0E-3 or less Signal peptide hits: Score= 0 or greater

Table 7 (cont.)

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, M. et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221.	Normalized quality score \geq GCG-specified "HIGH" value for that particular Prosite motif. Generally, score=1.4-2.1.
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M.S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12:431-439.	Score=3.5 or greater
TMAP	A program that uses weight matrices to delineate transmembrane segments on protein sequences and determine orientation.	Persson, B. and P. Argos (1994) J. Mol. Biol. 237:182-192; Persson, B. and P. Argos (1996) Protein Sci. 5:363-371.	
TMHMMER	A program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation.	Sonnhammer, E.L. et al. (1998) Proc. Sixth Intl. Conf. on Intelligent Systems for Mol. Biol., Glasgow et al., eds., The Am. Assoc. for Artificial Intelligence Press, Menlo Park, CA, pp. 175-182.	
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) Nucleic Acids Res. 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

What is claimed is:

1. An isolated polypeptide selected from the group consisting of:
 - a) a polypeptide comprising an amino acid sequence selected from the group consisting of
5 SEQ ID NO:1-21,
 - b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:1-21,
 - c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, and
10 d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21.
2. An isolated polypeptide of claim 1 selected from the group consisting of SEQ ID NO:1-
15 21.
3. An isolated polynucleotide encoding a polypeptide of claim 1.
4. An isolated polynucleotide encoding a polypeptide of claim 2.
- 20 5. An isolated polynucleotide of claim 4 selected from the group consisting of SEQ ID NO:22-42.
6. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 3.
25
7. A cell transformed with a recombinant polynucleotide of claim 6.
8. A transgenic organism comprising a recombinant polynucleotide of claim 6.
- 30 9. A method for producing a polypeptide of claim 1, the method comprising:
 - a) culturing a cell under conditions suitable for expression of the polypeptide, wherein said cell is transformed with a recombinant polynucleotide, and said recombinant polynucleotide comprises a promoter sequence operably linked to a polynucleotide encoding the polypeptide of claim 1, and
35 b) recovering the polypeptide so expressed.

10. An isolated antibody which specifically binds to a polypeptide of claim 1.

11. An isolated polynucleotide selected from the group consisting of:

- 5 a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:22-42,
b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:22-42,
c) a polynucleotide complementary to a polynucleotide of a),
d) a polynucleotide complementary to a polynucleotide of b), and
10 e) an RNA equivalent of a)-d).

12. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 11.

15 13. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:

- a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization
20 complex is formed between said probe and said target polynucleotide or fragments thereof, and
b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof.

25 14. A method of claim 13, wherein the probe comprises at least 60 contiguous nucleotides.

15. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 11, the method comprising:

- a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and
30 b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

35 16. A composition comprising a polypeptide of claim 1 and a pharmaceutically acceptable excipient.

17. A composition of claim 16, wherein the polypeptide has an amino acid sequence selected from the group consisting of SEQ ID NO:1-21.

18. A method for treating a disease or condition associated with decreased expression of functional PRTS, comprising administering to a patient in need of such treatment the composition of claim 16.

19. A method for screening a compound for effectiveness as an agonist of a polypeptide of claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting agonist activity in the sample.

20. A composition comprising an agonist compound identified by a method of claim 19 and a pharmaceutically acceptable excipient.

21. A method for treating a disease or condition associated with decreased expression of functional PRTS, comprising administering to a patient in need of such treatment a composition of claim 20.

22. A method for screening a compound for effectiveness as an antagonist of a polypeptide of claim 1, the method comprising:

- a) exposing a sample comprising a polypeptide of claim 1 to a compound, and
- b) detecting antagonist activity in the sample.

23. A composition comprising an antagonist compound identified by a method of claim 22 and a pharmaceutically acceptable excipient.

24. A method for treating a disease or condition associated with overexpression of functional PRTS, comprising administering to a patient in need of such treatment a composition of claim 23.

25. A method of screening for a compound that specifically binds to the polypeptide of claim 1, said method comprising the steps of:

- a) combining the polypeptide of claim 1 with at least one test compound under suitable conditions, and

b) detecting binding of the polypeptide of claim 1 to the test compound, thereby identifying a compound that specifically binds to the polypeptide of claim 1.

26. A method of screening for a compound that modulates the activity of the polypeptide of claim 1, said method comprising:

- a) combining the polypeptide of claim 1 with at least one test compound under conditions permissive for the activity of the polypeptide of claim 1,
- b) assessing the activity of the polypeptide of claim 1 in the presence of the test compound, and
- c) comparing the activity of the polypeptide of claim 1 in the presence of the test compound with the activity of the polypeptide of claim 1 in the absence of the test compound, wherein a change in the activity of the polypeptide of claim 1 in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide of claim 1.

27. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a sequence of claim 5, the method comprising:

- a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,
- b) detecting altered expression of the target polynucleotide, and
- c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

28. A method for assessing toxicity of a test compound, said method comprising:

- a) treating a biological sample containing nucleic acids with the test compound;
- b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 11 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 11 or fragment thereof;
- c) quantifying the amount of hybridization complex; and
- d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

29. A diagnostic test for a condition or disease associated with the expression of PRTS in a biological sample comprising the steps of:

- 5 a) combining the biological sample with an antibody of claim 10, under conditions suitable for the antibody to bind the polypeptide and form an antibody:polypeptide complex; and
 b) detecting the complex, wherein the presence of the complex correlates with the presence of the polypeptide in the biological sample.

30. The antibody of claim 10, wherein the antibody is:

- 10 a) a chimeric antibody,
 b) a single chain antibody,
 c) a Fab fragment,
 d) a F(ab')₂ fragment, or
15 e) a humanized antibody.

31. A composition comprising an antibody of claim 10 and an acceptable excipient.

32. A method of diagnosing a condition or disease associated with the expression of PRTS in a subject, comprising administering to said subject an effective amount of the composition of claim

20 31.

33. A composition of claim 31, wherein the antibody is labeled.

34. A method of diagnosing a condition or disease associated with the expression of PRTS in a subject, comprising administering to said subject an effective amount of the composition of claim

33.

35. A method of preparing a polyclonal antibody with the specificity of the antibody of claim 10 comprising:

- 30 a) immunizing an animal with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, or an immunogenic fragment thereof, under conditions to elicit an antibody response;
 b) isolating antibodies from said animal; and

c) screening the isolated antibodies with the polypeptide, thereby identifying a polyclonal antibody which binds specifically to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21.

5 36. An antibody produced by a method of claim 35.

37. A composition comprising the antibody of claim 36 and a suitable carrier.

38. A method of making a monoclonal antibody with the specificity of the antibody of claim
10 10 comprising:

a) immunizing an animal with a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21, or an immunogenic fragment thereof, under conditions to elicit an antibody response;

b) isolating antibody producing cells from the animal;

15 c) fusing the antibody producing cells with immortalized cells to form monoclonal antibody-producing hybridoma cells;

d) culturing the hybridoma cells; and

e) isolating from the culture monoclonal antibody which binds specifically to a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21.

20

39. A monoclonal antibody produced by a method of claim 38.

40. A composition comprising the antibody of claim 39 and a suitable carrier.

25 41. The antibody of claim 10, wherein the antibody is produced by screening a Fab expression library.

42. The antibody of claim 10, wherein the antibody is produced by screening a recombinant immunoglobulin library.

30

43. A method for detecting a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21 in a sample, comprising the steps of:

a) incubating the antibody of claim 10 with a sample under conditions to allow specific binding of the antibody and the polypeptide; and

b) detecting specific binding, wherein specific binding indicates the presence of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21 in the sample.

5 44. A method of purifying a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-21 from a sample, the method comprising:

a) incubating the antibody of claim 10 with a sample under conditions to allow specific binding of the antibody and the polypeptide; and
b) separating the antibody from the sample and obtaining the purified polypeptide having an
10 amino acid sequence selected from the group consisting of SEQ ID NO:1-21.

45. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:1.

15 46. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:2.

47. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:3.

20 48. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:4.

49. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:5.

50. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:6.

25 51. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:7.

52. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:8.

30 53. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:9.

54. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:10.

55. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:11.

56. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:12.
57. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:13.
- 5 58. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:14.
59. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:15.
60. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:16.
- 10 61. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:17.
62. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:18.
- 15 63. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:19.
64. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:20.
65. A polypeptide of claim 1, comprising the amino acid sequence of SEQ ID NO:21.
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67. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
25 NO:23.
68. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID
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71. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:27.

72. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:28.

73. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:29.

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75. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:31.

76. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:32.

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78. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:34.

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80. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:36.

81. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:37.

82. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:38.

5 83. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:39.

84. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:40.

10 85. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:41.

86. A polynucleotide of claim 11, comprising the polynucleotide sequence of SEQ ID NO:42.

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 TRIBOULEY, Catherine M.
 DELEGEANE, Angelo M.
 BAUGHN, Mariah R.
 NGUYEN, Danniel B.
 LEE, Ernestine A.
 HAFALIA, April
 KHAN, Farrah A.
 WALIA, Narinder K.
 YAO, Monique G.
 LU, Dyung Aina M.
 PATTERSON, Chandra
 TANG, Y. Tom
 WALSH, Roderick T.
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 Lys Thr Leu Asp Leu Arg Gly Arg Ala Gln Ala Leu Met Arg Ser
 80 85 90
 Phe Pro Leu Val Asp Gly His Asn Asp Leu Pro Gln Val Leu Arg
 95 100 105
 Gln Arg Tyr Lys Asn Val Leu Gln Asp Val Asn Leu Arg Asn Phe
 110 115 120
 Ser His Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val
 125 130 135
 Gly Ala Gln Phe Trp Ser Ala Ser Val Ser Cys Gln Ser Gln Asp
 140 145 150
 Gln Thr Ala Val Arg Leu Ala Leu Glu Gln Ile Asp Leu Ile His
 155 160 165
 Arg Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala
 170 175 180
 Glu Gly Leu Asn Ser Ser Gln Lys Leu Ala Cys Leu Ile Gly Val
 185 190 195
 Glu Gly Gly His Ser Leu Asp Ser Ser Leu Ser Val Leu Arg Ser
 200 205 210
 Phe Tyr Val Leu Gly Val Arg Tyr Leu Thr Leu Thr Phe Thr Cys
 215 220 225
 Ser Thr Pro Trp Ala Glu Ser Ser Thr Lys Phe Arg His His Met
 230 235 240
 Tyr Thr Asn Val Ser Gly Leu Thr Ser Phe Gly Glu Lys Val Val
 245 250 255
 Glu Glu Leu Asn Arg Leu Gly Met Met Ile Asp Leu Ser Tyr Ala
 260 265 270

Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro
 275 280 285
 Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu
 290 295 300
 Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Lys Asn Gly
 305 310 315
 Gly Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn
 320 325 330
 Leu Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile
 335 340 345
 Arg Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr
 350 355 360
 Asp Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr
 365 370 375
 Tyr Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Ser Trp Ser Glu
 380 385 390
 Glu Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe
 395 400 405
 Arg Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro
 410 415 420
 Val Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His
 425 430 435
 Ser His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu
 440 445 450
 Val Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn
 455 460 465
 Ala Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile
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 Pro Thr Phe Thr Gln Trp Leu Cys
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<210> 8

<211> 346

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 2256251CD1

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 Val Pro Lys Lys Ala Gly Arg Cys Gly Gln Gly Arg Leu His Gly
 20 25 30
 Gly Ser Ala Val Gly Phe Leu Gly Ser Pro Pro Gly Thr Pro Ser
 35 40 45
 Ser Phe Asp Leu Gly Cys Gly Arg Pro Gln Val Ser Asp Ala Gly
 50 55 60
 Gly Arg Ile Val Gly Gly His Ala Ala Pro Ala Gly Ala Trp Pro
 65 70 75
 Trp Gln Ala Ser Leu Arg Leu Arg Arg Val His Val Cys Gly Gly
 80 85 90
 Ser Leu Leu Ser Pro Gln Trp Val Leu Thr Ala Ala His Cys Phe
 95 100 105
 Ser Gly Ser Leu Asn Ser Ser Asp Tyr Gln Val His Leu Gly Glu
 110 115 120
 Leu Glu Ile Thr Leu Ser Pro His Phe Ser Thr Val Arg Gln Ile
 125 130 135
 Ile Leu His Ser Ser Pro Ser Gly Gln Pro Gly Thr Ser Gly Asp
 140 145 150
 Ile Ala Leu Val Glu Leu Ser Val Pro Val Thr Leu Phe Ser Arg
 155 160 165
 Ile Leu Pro Val Cys Leu Pro Glu Ala Ser Asp Asp Phe Cys Pro
 170 175 180
 Gly Ile Arg Cys Trp Val Thr Gly Trp Gly Tyr Thr Arg Glu Gly
 185 190 195

Glu	Pro	Leu	Pro	Pro	Pro	Tyr	Ser	Leu	Arg	Glu	Val	Lys	Val	Ser	
				200					205					210	
Val	Val	Asp	Thr	Glu	Thr	Cys	Arg	Arg	Asp	Tyr	Pro	Gly	Pro	Gly	
				215					220					225	
Gly	Ser	Ile	Leu	Gln	Pro	Asp	Met	Leu	Cys	Ala	Arg	Gly	Pro	Gly	
				230					235					240	
Asp	Ala	Cys	Gln	Asp	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gln	Val	
				245					250					255	
Asn	Gly	Ala	Trp	Val	Gln	Ala	Gly	Ile	Val	Ser	Trp	Gly	Glu	Gly	
				260					265					270	
Cys	Gly	Arg	Pro	Asn	Arg	Pro	Gly	Val	Tyr	Thr	Arg	Val	Pro	Ala	
				275					280					285	
Tyr	Val	Asn	Trp	Ile	Arg	Arg	His	Ile	Thr	Ala	Ser	Gly	Gly	Ser	
				290					295					300	
Glu	Ser	Gly	Tyr	Pro	Arg	Leu	Pro	Leu	Leu	Ala	Gly	Leu	Phe	Leu	
				305					310					315	
Pro	Gly	Leu	Phe	Leu	Leu	Leu	Val	Ser	Cys	Val	Leu	Leu	Ala	Lys	
				320					325					330	
Cys	Leu	Leu	His	Pro	Ser	Ala	Asp	Gly	Thr	Pro	Phe	Pro	Ala	Pro	
				335					340					345	
Asp															

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<211> 882

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7160544CD1

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Glu	Thr	Ala	Asp	Cys	Glu	Glu	Asn	Ile	Glu	Ser	Gln	Asp	Arg	Pro	
				20					25					30	
Lys	Leu	Glu	Pro	Phe	Tyr	Val	Glu	Arg	Tyr	Ser	Trp	Ser	Gln	Leu	
				35					40					45	
Lys	Lys	Leu	Leu	Ala	Asp	Thr	Arg	Lys	Tyr	His	Gly	Tyr	Met	Met	
				50					55					60	
Ala	Lys	Ala	Pro	His	Asp	Phe	Met	Phe	Val	Lys	Arg	Asn	Asp	Pro	
				65					70					75	
Asp	Gly	Pro	His	Ser	Asp	Arg	Ile	Tyr	Tyr	Leu	Ala	Met	Ser	Gly	
				80					85					90	
Glu	Asn	Arg	Glu	Asn	Thr	Leu	Phe	Tyr	Ser	Glu	Ile	Pro	Lys	Thr	
				95					100					105	
Ile	Asn	Arg	Ala	Ala	Val	Leu	Met	Leu	Ser	Trp	Lys	Pro	Leu	Leu	
				110					115					120	
Asp	Leu	Phe	Gln	Ala	Thr	Leu	Asp	Tyr	Gly	Met	Tyr	Ser	Arg	Glu	
				125					130					135	
Glu	Glu	Leu	Leu	Arg	Glu	Arg	Lys	Arg	Ile	Gly	Thr	Val	Gly	Ile	
				140					145					150	
Ala	Ser	Tyr	Asp	Tyr	His	Gln	Gly	Ser	Gly	Thr	Phe	Leu	Phe	Gln	
				155					160					165	
Ala	Gly	Ser	Gly	Ile	Tyr	His	Val	Lys	Asp	Gly	Gly	Pro	Gln	Gly	
				170					175					180	
Phe	Thr	Gln	Gln	Pro	Leu	Arg	Pro	Asn	Leu	Val	Glu	Thr	Ser	Cys	
				185					190					195	
Pro	Asn	Ile	Arg	Met	Asp	Pro	Lys	Leu	Cys	Pro	Ala	Asp	Pro	Asp	
				200					205					210	
Trp	Ile	Ala	Phe	Ile	His	Ser	Asn	Asp	Ile	Trp	Ile	Ser	Asn	Ile	
				215					220					225	
Val	Thr	Arg	Glu	Glu	Arg	Arg	Leu	Thr	Tyr	Val	His	Asn	Glu	Leu	
				230					235					240	
Ala	Asn	Met	Glu	Glu	Asp	Ala	Arg	Ser	Ala	Gly	Val	Ala	Thr	Phe	
				245					250					255	

Val	Leu	Gln	Glu	Glu	Phe	Asp	Arg	Tyr	Ser	Gly	Tyr	Trp	Trp	Cys
				260					265					270
Pro	Lys	Ala	Glu	Thr	Thr	Pro	Ser	Gly	Gly	Lys	Ile	Leu	Arg	Ile
				275					280					285
Leu	Tyr	Glu	Glu	Asn	Asp	Glu	Ser	Glu	Val	Glu	Ile	Ile	His	Val
				290					295					300
Thr	Ser	Pro	Met	Leu	Glu	Thr	Arg	Arg	Ala	Asp	Ser	Phe	Arg	Tyr
				305					310					315
Pro	Lys	Thr	Gly	Thr	Ala	Asn	Pro	Lys	Val	Thr	Phe	Lys	Met	Ser
				320					325					330
Glu	Ile	Met	Ile	Asp	Ala	Glu	Gly	Arg	Ile	Ile	Asp	Val	Ile	Asp
				335					340					345
Lys	Glu	Leu	Ile	Gln	Pro	Phe	Glu	Ile	Leu	Phe	Glu	Gly	Val	Glu
				350					355					360
Tyr	Ile	Ala	Arg	Ala	Gly	Trp	Thr	Pro	Glu	Gly	Lys	Tyr	Ala	Trp
				365					370					375
Ser	Ile	Leu	Leu	Asp	Arg	Ser	Gln	Thr	Arg	Leu	Gln	Ile	Val	Leu
				380					385					390
Ile	Ser	Pro	Glu	Leu	Phe	Ile	Pro	Val	Glu	Asp	Asp	Val	Met	Glu
				395					400					405
Arg	Gln	Arg	Leu	Ile	Glu	Ser	Val	Pro	Asp	Ser	Val	Thr	Pro	Leu
				410					415					420
Ile	Ile	Tyr	Glu	Glu	Thr	Thr	Asp	Ile	Trp	Ile	Asn	Ile	His	Asp
				425					430					435
Ile	Phe	His	Val	Phe	Pro	Gln	Ser	His	Glu	Glu	Glu	Ile	Glu	Phe
				440					445					450
Ile	Phe	Ala	Ser	Glu	Cys	Lys	Thr	Gly	Phe	Arg	His	Leu	Tyr	Lys
				455					460					465
Ile	Thr	Ser	Ile	Leu	Lys	Glu	Ser	Lys	Tyr	Lys	Arg	Ser	Ser	Gly
				470					475					480
Gly	Leu	Pro	Ala	Pro	Ser	Asp	Phe	Lys	Cys	Pro	Ile	Lys	Glu	Glu
				485					490					495
Ile	Ala	Ile	Thr	Ser	Gly	Glu	Trp	Glu	Val	Leu	Gly	Arg	His	Gly
				500					505					510
Ser	Asn	Ile	Gln	Val	Asp	Glu	Val	Arg	Arg	Leu	Val	Tyr	Phe	Glu
				515					520					525
Gly	Thr	Lys	Asp	Ser	Pro	Leu	Glu	His	His	Leu	Tyr	Val	Val	Ser
				530					535					540
Tyr	Val	Asn	Pro	Gly	Glu	Val	Thr	Arg	Leu	Thr	Asp	Arg	Gly	Tyr
				545					550					555
Ser	His	Ser	Cys	Cys	Ile	Ser	Gln	His	Cys	Asp	Phe	Phe	Ile	Ser
				560					565					570
Lys	Tyr	Ser	Asn	Gln	Lys	Asn	Pro	His	Cys	Val	Ser	Leu	Tyr	Lys
				575					580					585
Leu	Ser	Ser	Pro	Glu	Asp	Asp	Pro	Thr	Cys	Lys	Thr	Lys	Glu	Phe
				590					595					600
Trp	Ala	Thr	Ile	Leu	Asp	Ser	Ala	Gly	Pro	Leu	Pro	Asp	Tyr	Thr
				605					610					615
Pro	Pro	Glu	Ile	Phe	Ser	Phe	Glu	Ser	Thr	Thr	Gly	Phe	Thr	Leu
				620					625					630
Tyr	Gly	Met	Leu	Tyr	Lys	Pro	His	Asp	Leu	Gln	Pro	Gly	Lys	Lys
				635					640					645
Tyr	Pro	Thr	Val	Leu	Phe	Ile	Tyr	Gly	Gly	Pro	Gln	Val	Gln	Leu
				650					655					660
Val	Asn	Asn	Arg	Phe	Lys	Gly	Val	Lys	Tyr	Phe	Arg	Leu	Asn	Thr
				665					670					675
Leu	Ala	Ser	Leu	Gly	Tyr	Val	Val	Val	Val	Ile	Asp	Asn	Arg	Gly
				680					685					690
Ser	Cys	His	Arg	Gly	Leu	Lys	Phe	Glu	Gly	Ala	Phe	Lys	Tyr	Lys
				695					700					705
Met	Gly	Gln	Ile	Glu	Ile	Asp	Asp	Gln	Val	Glu	Gly	Leu	Gln	Tyr
				710					715					720
Leu	Ala	Ser	Arg	Tyr	Asp	Phe	Ile	Asp	Leu	Asp	Arg	Val	Gly	Ile
				725					730					735
His	Gly	Trp	Ser	Tyr	Gly	Gly	Tyr	Leu	Ser	Leu	Met	Ala	Leu	Met
				740					745					750
Gln	Arg	Ser	Asp	Ile	Phe	Arg	Val	Ala	Ile	Ala	Gly	Ala	Pro	Val

Thr Leu Trp Ile	755	Phe Tyr Asp Thr Gly	760	Tyr Thr Glu Arg Tyr	765
Gly His Pro Asp	770	Gln Asn Glu Gln Gly	775	Tyr Tyr Leu Gly Ser	780
Ala Met Gln Ala	785	Glu Lys Phe Pro Ser	790	Glu Pro Asn Arg Leu	795
Leu Leu His Gly	800	Phe Leu Asp Glu Asn	805	Val His Phe Ala His	810
Ser Ile Leu Leu	815	Ser Phe Leu Val Arg	820	Ala Gly Lys Pro Tyr	825
Leu Gln Ile Tyr	830	Pro Gln Glu Arg His	835	Ser Ile Arg Val Pro	840
Ser Gly Glu His	845	Tyr Glu Leu His Leu	850	Leu His Tyr Leu Gln	855
Asn Leu Gly Ser	860	Arg Ile Ala Ala Leu	865	Lys Val Ile	870
	875		880		

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<211> 1189

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7477386CD1

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Cys Ala Leu Cys Ala	20	Ala Ala Gly Ser Arg	25	Thr Pro Glu Leu His	30
Leu Ser Gly Lys Leu	35	Ser Asp Tyr Gly Val	40	Thr Val Pro Cys Ser	45
Thr Asp Phe Arg Gly	50	Arg Phe Leu Ser His	55	Val Val Ser Gly Pro	60
Ala Ala Ala Ser Ala	65	Gly Ser Met Val Val	70	Asp Thr Pro Pro Thr	75
Leu Pro Arg His Ser	80	Ser His Leu Arg Val	85	Ala Arg Ser Pro Leu	90
His Pro Gly Gly Thr	95	Leu Trp Pro Gly Arg	100	Val Gly Arg His Ser	105
Leu Tyr Phe Asn Val	110	Thr Val Phe Gly Lys	115	Glu Leu His Leu Arg	120
Leu Arg Pro Asn Arg	125	Arg Leu Val Val Pro	130	Gly Ser Ser Val Glu	135
Trp Gln Glu Asp Phe	140	Arg Glu Leu Phe Arg	145	Gln Pro Leu Arg Gln	150
Glu Cys Val Tyr Thr	155	Gly Gly Val Thr Gly	160	Met Pro Gly Ala Ala	165
Val Ala Ile Ser Asn	170	Cys Asp Gly Leu Ala	175	Gly Leu Ile Arg Thr	180
Asp Ser Thr Asp Phe	185	Phe Ile Glu Pro Leu	190	Glu Arg Gly Gln Gln	195
Glu Lys Glu Ala Ser	200	Gly Arg Thr His Val	205	Val Tyr Arg Arg Glu	210
Ala Val Gln Gln Glu	215	Trp Ala Glu Pro Asp	220	Gly Asp Leu His Asn	225
Glu Ala Phe Gly Leu	230	Gly Asp Leu Pro Asn	235	Leu Leu Gly Leu Val	240
Gly Asp Gln Leu Gly	245	Asp Thr Glu Arg Lys	250	Arg Arg His Ala Lys	255
Pro Gly Ser Tyr Ser	260	Ile Glu Val Leu Leu	265	Val Val Asp Asp Ser	270
Val Val Arg Phe His	275	Gly Lys Glu His Val	280	Gln Asn Tyr Val Leu	285
Thr Leu Met Asn Ile		Val Val Asp Glu Ile		Tyr His Asp Glu Ser	

Leu Gly Val His	290	Ile Asn Ile Ala Leu	295	Val Arg Leu Ile Met	300
	305		310		315
Gly Tyr Arg Gln	320	Gln Ser Leu Ser Leu	325	Ile Glu Arg Gly Asn Pro	330
Ser Arg Ser Leu	335	Glu Gln Val Cys Arg	340	Trp Ala His Ser Gln Gln	345
Arg Gln Asp Pro	350	Ser His Ala Glu His	355	His Asp His Val Val Phe	360
Leu Thr Arg Gln	365	Asp Phe Gly Pro Ser	370	Gly Gly Tyr Ala Pro Val	375
Thr Gly Met Cys	380	His Pro Leu Arg Ser	385	Cys Ala Leu Asn His Glu	390
Asp Gly Phe Ser	395	Ser Ala Phe Val Ile	400	Ala His Glu Thr Gly His	405
Val Leu Gly Met	410	Glu His Asp Gly Gln	415	Gly Asn Gly Cys Ala Asp	420
Glu Thr Ser Leu	425	Gly Ser Val Met Ala	430	Pro Leu Val Gln Ala Ala	435
Phe His Arg Phe	440	His Trp Ser Arg Cys	445	Ser Lys Leu Glu Leu Ser	450
Arg Tyr Leu Pro	455	Ser Tyr Asp Cys Leu	460	Leu Asp Asp Pro Phe Asp	465
Pro Ala Trp Pro	470	Gln Pro Pro Glu Leu	475	Pro Gly Ile Asn Tyr Ser	480
Met Asp Glu Gln	485	Cys Arg Phe Asp Phe	490	Gly Ser Gly Tyr Gln Thr	495
Cys Leu Ala Phe	500	Arg Thr Phe Glu Pro	505	Cys Lys Gln Leu Trp Cys	510
Ser His Pro Asp	515	Asn Pro Tyr Phe Cys	520	Lys Thr Lys Lys Gly Pro	525
Pro Leu Asp Gly	530	Thr Glu Cys Ala Pro	535	Gly Lys Trp Cys Phe Lys	540
Gly His Cys Ile	545	Trp Lys Ser Pro Glu	550	Gln Thr Tyr Gly Gln Asp	555
Gly Gly Trp Ser	560	Ser Trp Thr Lys Phe	565	Gly Ser Cys Ser Arg Ser	570
Cys Gly Gly Gly	575	Val Arg Ser Arg Ser	580	Arg Ser Cys Asn Asn Pro	585
Ser Pro Ala Tyr	590	Gly Gly Arg Leu Cys	595	Leu Gly Pro Met Phe Glu	600
Tyr Gln Val Cys	605	Asn Ser Glu Glu Cys	610	Pro Gly Thr Tyr Glu Asp	615
Phe Arg Ala Gln	620	Gln Cys Ala Lys Arg	625	Asn Ser Tyr Tyr Val His	630
Gln Asn Ala Lys	635	His Ser Trp Val Pro	640	Tyr Glu Pro Asp Asp Asp	645
Ala Gln Lys Cys	650	Glu Leu Ile Cys Gln	655	Ser Ala Asp Thr Gly Asp	660
Val Val Phe Met	665	Asn Gln Val Val His	670	Asp Gly Thr Arg Cys Ser	675
Tyr Arg Asp Pro	680	Tyr Ser Val Cys Ala	685	Arg Gly Glu Cys Val Pro	690
Val Gly Cys Asp	695	Lys Glu Val Gly Ser	700	Met Lys Ala Asp Asp Lys	705
Cys Gly Val Cys	710	Gly Gly Asp Asn Ser	715	His Cys Arg Thr Val Lys	720
Gly Thr Leu Gly	725	Lys Ala Ser Lys Gln	730	Ala Gly Ala Leu Lys Leu	735
Val Gln Ile Pro	740	Ala Gly Ala Arg His	745	Ile Gln Ile Glu Ala Leu	750
Glu Lys Ser Pro	755	His Arg Ile Val Val	760	Lys Asn Gln Val Thr Gly	765
Ser Phe Ile Leu	770	Asn Pro Lys Gly Lys	775	Glu Ala Thr Ser Arg Thr	780
Phe Thr Ala Met	785	Gly Leu Glu Trp Glu	790	Asp Ala Val Glu Asp Ala	795

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Met  Leu  Leu  Leu  Gly  Ile  Leu  Thr  Leu  Ala  Phe  Ala  Gly  Arg  Thr
  1          5          10          15
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Ala Gly Gly Ser	Glu	Pro	Glu	Arg	Glu	Val	Val	Val	Pro	Ile	Arg	
	20					25					30	
Leu Asp Pro Asp	Ile	Asn	Gly	Arg	Arg	Tyr	Tyr	Trp	Arg	Gly	Pro	
	35					40					45	
Glu Asp Ser Gly	Asp	Gln	Gly	Leu	Ile	Phe	Gln	Ile	Thr	Ala	Phe	
	50					55					60	
Gln Glu Asp Phe	Tyr	Leu	His	Leu	Thr	Pro	Asp	Ala	Gln	Phe	Leu	
	65					70					75	
Ala Pro Ala Phe	Ser	Thr	Glu	His	Leu	Gly	Val	Pro	Leu	Gln	Gly	
	80					85					90	
Leu Thr Gly Gly	Ser	Ser	Asp	Leu	Arg	Arg	Cys	Phe	Tyr	Ser	Gly	
	95					100					105	
Asp Val Asn Ala	Glu	Pro	Asp	Ser	Phe	Ala	Ala	Val	Ser	Leu	Cys	
	110					115					120	
Gly Gly Leu Arg	Gly	Ala	Phe	Gly	Tyr	Arg	Gly	Ala	Glu	Tyr	Val	
	125					130					135	
Ile Ser Pro Leu	Pro	Asn	Ala	Ser	Ala	Pro	Ala	Ala	Gln	Arg	Asn	
	140					145					150	
Ser Gln Gly Ala	His	Leu	Leu	Gln	Arg	Arg	Gly	Val	Pro	Gly	Gly	
	155					160					165	
Pro Ser Gly Asp	Pro	Thr	Ser	Arg	Cys	Gly	Val	Ala	Ser	Gly	Trp	
	170					175					180	
Asn Pro Ala Ile	Leu	Arg	Ala	Leu	Asp	Pro	Tyr	Lys	Pro	Arg	Arg	
	185					190					195	
Ala Gly Phe Gly	Glu	Ser	Arg	Ser	Arg	Arg	Arg	Ser	Gly	Arg	Ala	
	200					205					210	
Lys Arg Phe Val	Ser	Ile	Pro	Arg	Tyr	Val	Glu	Thr	Leu	Val	Val	
	215					220					225	
Ala Asp Glu Ser	Met	Val	Lys	Phe	His	Gly	Ala	Asp	Leu	Glu	His	
	230					235					240	
Tyr Leu Leu Thr	Leu	Leu	Ala	Thr	Ala	Ala	Arg	Leu	Tyr	Arg	His	
	245					250					255	
Pro Ser Ile Leu	Asn	Pro	Ile	Asn	Ile	Val	Val	Val	Lys	Val	Leu	
	260					265					270	
Leu Leu Arg Asp	Arg	Asp	Ser	Gly	Pro	Lys	Val	Thr	Gly	Asn	Ala	
	275					280					285	
Ala Leu Thr Leu	Arg	Asn	Phe	Cys	Ala	Trp	Gln	Lys	Lys	Leu	Asn	
	290					295					300	
Lys Val Ser Asp	Lys	His	Pro	Glu	Tyr	Trp	Asp	Thr	Ala	Ile	Leu	
	305					310					315	
Phe Thr Arg Gln	Asp	Leu	Cys	Gly	Ala	Thr	Thr	Cys	Asp	Thr	Leu	
	320					325					330	
Gly Met Ala Asp	Val	Gly	Thr	Met	Cys	Asp	Pro	Lys	Arg	Ser	Cys	
	335					340					345	
Ser Val Ile Glu	Asp	Asp	Gly	Leu	Pro	Ser	Ala	Phe	Thr	Thr	Ala	
	350					355					360	
His Glu Leu Gly	His	Val	Phe	Asn	Met	Pro	His	Asp	Asn	Val	Lys	
	365					370					375	
Val Cys Glu Glu	Val	Phe	Gly	Lys	Leu	Arg	Ala	Asn	His	Met	Met	
	380					385					390	
Ser Pro Thr Leu	Ile	Gln	Ile	Asp	Arg	Ala	Asn	Pro	Trp	Ser	Ala	
	395					400					405	
Cys Ser Ala Ala	Ile	Ile	Thr	Asp	Phe	Leu	Asp	Ser	Gly	His	Gly	
	410					415					420	
Asp Cys Leu Leu	Asp	Gln	Pro	Ser	Lys	Pro	Ile	Ser	Leu	Pro	Glu	
	425					430					435	
Asp Leu Pro Gly	Ala	Ser	Tyr	Thr	Leu	Ser	Gln	Gln	Cys	Glu	Leu	
	440					445					450	
Ala Phe Gly Val	Gly	Ser	Lys	Pro	Cys	Pro	Tyr	Met	Gln	Tyr	Cys	
	455					460					465	
Thr Lys Leu Trp	Cys	Thr	Gly	Lys	Ala	Lys	Gly	Gln	Met	Val	Cys	
	470					475					480	
Gln Thr Arg His	Phe	Pro	Trp	Ala	Asp	Gly	Thr	Ser	Cys	Gly	Glu	
	485					490					495	
Gly Lys Leu Cys	Leu	Lys	Gly	Ala	Cys	Val	Glu	Arg	His	Asn	Leu	
	500					505					510	
Asn Lys His Arg	Val	Asp	Gly	Ser	Trp	Ala	Lys	Trp	Asp	Pro	Tyr	

Gly	Pro	Cys	Ser	515	Arg	Thr	Cys	Gly	Gly	520	Gly	Val	Gln	Leu	Ala	Arg	525
Arg	Gln	Cys	Thr	530	Asn	Pro	Thr	Pro	Ala	535	Asn	Gly	Gly	Lys	Tyr	Cys	540
Glu	Gly	Val	Arg	545	Val	Lys	Tyr	Arg	Ser	550	Cys	Asn	Leu	Glu	Pro	Cys	555
Pro	Ser	Ser	Ala	560	Ser	Gly	Lys	Ser	Phe	565	Arg	Glu	Glu	Gln	Cys	Glu	570
Ala	Phe	Asn	Gly	575	Tyr	Asn	His	Ser	Thr	580	Asn	Arg	Leu	Thr	Leu	Ala	585
Val	Ala	Trp	Val	590	Pro	Lys	Tyr	Ser	Gly	595	Val	Ser	Pro	Arg	Asp	Lys	600
Cys	Lys	Leu	Ile	605	Cys	Arg	Ala	Asn	Gly	610	Thr	Gly	Tyr	Phe	Tyr	Val	615
Leu	Ala	Pro	Lys	620	Val	Val	Val	Asp	Gly	625	Thr	Leu	Cys	Ser	Pro	Asp	630
Ser	Thr	Ser	Val	635	Cys	Val	Gln	Gly	Lys	640	Cys	Ile	Lys	Ala	Gly	Cys	645
Asp	Gly	Asn	Leu	650	Gly	Ser	Lys	Lys	Arg	655	Phe	Asp	Lys	Cys	Gly	Val	660
Cys	Gly	Gly	Asp	665	Asn	Lys	Ser	Cys	Lys	670	Lys	Val	Thr	Gly	Leu	Phe	675
Thr	Lys	Pro	Met	680	His	Gly	Tyr	Asn	Phe	685	Val	Val	Ala	Ile	Pro	Ala	690
Gly	Ala	Ser	Ser	695	Ile	Asp	Ile	Arg	Gln	700	Arg	Gly	Tyr	Lys	Gly	Leu	705
Ile	Gly	Asp	Asp	710	Asn	Tyr	Leu	Ala	Leu	715	Lys	Asn	Ser	Gln	Gly	Lys	720
Tyr	Leu	Leu	Asn	725	Gly	His	Phe	Val	Val	730	Ser	Ala	Val	Glu	Arg	Asp	735
Leu	Val	Val	Lys	740	Gly	Ser	Leu	Leu	Arg	745	Tyr	Ser	Gly	Thr	Gly	Thr	750
Ala	Val	Glu	Ser	755	Leu	Gln	Ala	Ser	Arg	760	Pro	Ile	Leu	Glu	Pro	Leu	765
Thr	Val	Glu	Val	770	Leu	Ser	Val	Gly	Lys	775	Met	Thr	Pro	Pro	Arg	Val	780
Arg	Tyr	Ser	Phe	785	Tyr	Leu	Pro	Lys	Glu	790	Pro	Arg	Glu	Asp	Lys	Ser	795
Ser	His	Pro	Pro	800	His	Pro	Arg	Gly	Gly	805	Pro	Ser	Val	Leu	His	Asn	810
Ser	Val	Leu	Ser	815	Leu	Ser	Asn	Gln	Val	820	Glu	Gln	Pro	Asp	Asp	Arg	825
Pro	Pro	Ala	Arg	830	Trp	Val	Ala	Gly	Ser	835	Trp	Gly	Pro	Cys	Ser	Ala	840
Ser	Cys	Gly	Ser	845	Gly	Leu	Gln	Lys	Arg	850	Ala	Val	Asp	Trp	Arg	Gly	855
Ser	Ala	Gly	Gln	860	Arg	Thr	Val	Pro	Ala	865	Cys	Asp	Ala	Ala	His	Arg	870
Pro	Val	Glu	Thr	875	Gln	Ala	Cys	Gly	Glu	880	Pro	Cys	Pro	Thr	Trp	Glu	885
Leu	Ser	Ala	Trp	890	Ser	Pro	Cys	Ser	Lys	895	Ser	Cys	Gly	Arg	Gly	Phe	900
Gln	Arg	Arg	Ser	905	Leu	Lys	Cys	Val	Gly	910	His	Gly	Gly	Arg	Leu	Leu	915
Ala	Arg	Asp	Gln	920	Cys	Asn	Leu	His	Arg	925	Lys	Pro	Gln	Glu	Leu	Asp	930
Phe	Cys	Val	Leu	935	Arg	Pro	Cys			940							945
				950													

<210> 12
 <211> 898
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature

<223> Incyte ID No: 7604035CD1

<400> 12

Met	Glu	Asn	Trp	Thr	Gly	Arg	Pro	Trp	Leu	Tyr	Leu	Leu	Leu	Leu	15
1				5					10						15
Leu	Ser	Leu	Pro	Gln	Leu	Cys	Leu	Asp	Gln	Glu	Val	Leu	Ser	Gly	30
				20					25						30
His	Ser	Leu	Gln	Thr	Pro	Thr	Glu	Glu	Gly	Gln	Gly	Pro	Glu	Gly	45
				35					40						45
Val	Trp	Gly	Pro	Trp	Val	Gln	Trp	Ala	Ser	Cys	Ser	Gln	Pro	Cys	60
				50					55						60
Gly	Val	Gly	Val	Gln	Arg	Arg	Ser	Arg	Thr	Cys	Gln	Leu	Pro	Thr	75
				65					70						75
Val	Gln	Leu	His	Pro	Ser	Leu	Pro	Leu	Pro	Pro	Arg	Pro	Pro	Arg	90
				80					85						90
His	Pro	Glu	Ala	Leu	Leu	Pro	Arg	Gly	Gln	Gly	Pro	Arg	Pro	Gln	105
				95					100						105
Thr	Ser	Pro	Glu	Thr	Leu	Pro	Leu	Tyr	Arg	Thr	Gln	Ser	Arg	Gly	120
				110					115						120
Arg	Gly	Gly	Pro	Leu	Arg	Gly	Pro	Ala	Ser	His	Leu	Gly	Arg	Glu	135
				125					130						135
Glu	Thr	Gln	Glu	Ile	Arg	Ala	Ala	Arg	Arg	Ser	Arg	Leu	Arg	Asp	150
				140					145						150
Pro	Ile	Lys	Pro	Gly	Met	Phe	Gly	Tyr	Gly	Arg	Val	Pro	Phe	Ala	165
				155					160						165
Leu	Pro	Leu	His	Arg	Asn	Arg	Arg	His	Pro	Arg	Ser	Pro	Pro	Arg	180
				170					175						180
Ser	Glu	Leu	Ser	Leu	Ile	Ser	Ser	Arg	Gly	Glu	Glu	Pro	Ile	Pro	195
				185					190						195
Ser	Pro	Thr	Pro	Arg	Ala	Glu	Pro	Phe	Ser	Ala	Asn	Gly	Ser	Pro	210
				200					205						210
Gln	Thr	Glu	Leu	Pro	Pro	Thr	Glu	Leu	Ser	Val	His	Thr	Pro	Ser	225
				215					220						225
Pro	Gln	Ala	Glu	Pro	Leu	Ser	Pro	Glu	Thr	Ala	Gln	Thr	Glu	Val	240
				230					235						240
Ala	Pro	Arg	Thr	Arg	Pro	Ala	Pro	Leu	Arg	His	His	Pro	Arg	Ala	255
				245					250						255
Gln	Ala	Ser	Gly	Thr	Glu	Pro	Pro	Ser	Pro	Thr	His	Ser	Leu	Gly	270
				260					265						270
Glu	Gly	Gly	Phe	Phe	Arg	Ala	Ser	Pro	Gln	Pro	Arg	Arg	Pro	Ser	285
				275					280						285
Ser	Gln	Gly	Trp	Ala	Ser	Pro	Gln	Val	Ala	Gly	Arg	Arg	Pro	Asp	300
				290					295						300
Pro	Phe	Pro	Ser	Val	Pro	Arg	Gly	Arg	Gly	Gln	Gln	Gly	Gln	Gly	315
				305					310						315
Pro	Trp	Gly	Thr	Gly	Gly	Thr	Pro	His	Gly	Pro	Arg	Leu	Glu	Pro	330
				320					325						330
Asp	Pro	Gln	His	Pro	Gly	Ala	Trp	Leu	Pro	Leu	Leu	Ser	Asn	Gly	345
				335					340						345
Pro	His	Ala	Ser	Ser	Leu	Trp	Ser	Leu	Phe	Ala	Pro	Ser	Ser	Pro	360
				350					355						360
Ile	Pro	Arg	Cys	Ser	Gly	Glu	Ser	Glu	Gln	Leu	Arg	Ala	Cys	Ser	375
				365					370						375
Gln	Ala	Pro	Cys	Pro	Pro	Glu	Gln	Pro	Asp	Pro	Arg	Ala	Leu	Gln	390
				380					385						390
Cys	Ala	Ala	Phe	Asn	Ser	Gln	Glu	Phe	Met	Gly	Gln	Leu	Tyr	Gln	405
				395					400						405
Trp	Glu	Pro	Phe	Thr	Glu	Val	Gln	Gly	Ser	Gln	Arg	Cys	Glu	Leu	420
				410					415						420
Asn	Cys	Arg	Pro	Arg	Gly	Phe	Arg	Phe	Tyr	Val	Arg	His	Thr	Glu	435
				425					430						435
Lys	Val	Gln	Asp	Gly	Thr	Leu	Cys	Gln	Pro	Gly	Ala	Pro	Asp	Ile	450
				440					445						450
Cys	Val	Ala	Gly	Arg	Cys	Leu	Ser	Pro	Gly	Cys	Asp	Gly	Ile	Leu	465
				455					460						465
Gly	Ser	Gly	Arg	Arg	Pro	Asp	Gly	Cys	Gly	Val	Cys	Gly	Gly	Asp	480
				470					475						480

Asp	Ser	Thr	Cys	Arg	Leu	Val	Ser	Gly	Asn	Leu	Thr	Asp	Arg	Gly	485	490	495
Gly	Pro	Leu	Gly	Tyr	Gln	Lys	Ile	Leu	Trp	Ile	Pro	Ala	Gly	Ala	500	505	510
Leu	Arg	Leu	Gln	Ile	Ala	Gln	Leu	Arg	Pro	Ser	Ser	Asn	Tyr	Leu	515	520	525
Ala	Leu	Arg	Gly	Pro	Gly	Gly	Arg	Ser	Ile	Ile	Asn	Gly	Asn	Trp	530	535	540
Ala	Val	Asp	Pro	Pro	Gly	Ser	Tyr	Arg	Ala	Gly	Gly	Thr	Val	Phe	545	550	555
Arg	Tyr	Asn	Arg	Pro	Pro	Arg	Glu	Glu	Gly	Lys	Gly	Glu	Ser	Leu	560	565	570
Ser	Ala	Glu	Gly	Pro	Thr	Thr	Gln	Pro	Val	Asp	Val	Tyr	Met	Ile	575	580	585
Phe	Gln	Glu	Glu	Asn	Pro	Gly	Val	Phe	Tyr	Gln	Tyr	Val	Ile	Ser	590	595	600
Ser	Pro	Pro	Pro	Ile	Leu	Glu	Asn	Pro	Thr	Pro	Glu	Pro	Pro	Val	605	610	615
Pro	Gln	Leu	Gln	Pro	Glu	Ile	Leu	Arg	Val	Glu	Pro	Pro	Leu	Ala	620	625	630
Pro	Ala	Pro	Arg	Pro	Ala	Arg	Thr	Pro	Gly	Thr	Leu	Gln	Arg	Gln	635	640	645
Val	Arg	Ile	Pro	Gln	Met	Pro	Ala	Pro	Pro	His	Pro	Arg	Thr	Pro	650	655	660
Leu	Gly	Ser	Pro	Ala	Ala	Tyr	Trp	Lys	Arg	Val	Gly	His	Ser	Ala	665	670	675
Cys	Ser	Ala	Ser	Cys	Gly	Lys	Gly	Val	Trp	Arg	Pro	Ile	Phe	Leu	680	685	690
Cys	Ile	Ser	Arg	Glu	Ser	Gly	Glu	Glu	Leu	Asp	Glu	Arg	Ser	Cys	695	700	705
Ala	Ala	Gly	Ala	Arg	Pro	Pro	Ala	Ser	Pro	Glu	Pro	Cys	His	Gly	710	715	720
Thr	Pro	Cys	Pro	Pro	Tyr	Trp	Glu	Ala	Gly	Glu	Trp	Thr	Ser	Cys	725	730	735
Ser	Arg	Ser	Cys	Gly	Pro	Gly	Thr	Gln	His	Arg	Gln	Leu	Gln	Cys	740	745	750
Arg	Gln	Glu	Phe	Gly	Gly	Gly	Gly	Ser	Ser	Val	Pro	Pro	Glu	Arg	755	760	765
Cys	Gly	His	Leu	Pro	Arg	Pro	Asn	Ile	Thr	Gln	Ser	Cys	Gln	Leu	770	775	780
Arg	Leu	Cys	Gly	His	Trp	Glu	Val	Gly	Ser	Pro	Trp	Ser	Gln	Cys	785	790	795
Ser	Val	Arg	Cys	Gly	Arg	Gly	Gln	Arg	Ser	Arg	Gln	Val	Arg	Cys	800	805	810
Val	Gly	Asn	Asn	Gly	Asp	Glu	Val	Ser	Glu	Gln	Glu	Cys	Ala	Ser	815	820	825
Gly	Pro	Pro	Gln	Pro	Pro	Ser	Arg	Glu	Ala	Cys	Asp	Met	Gly	Pro	830	835	840
Cys	Thr	Thr	Ala	Trp	Phe	His	Ser	Asp	Trp	Ser	Ser	Lys	Cys	Ser	845	850	855
Ala	Glu	Cys	Gly	Thr	Gly	Ile	Gln	Arg	Arg	Ser	Val	Val	Cys	Leu	860	865	870
Gly	Ser	Gly	Ala	Ala	Thr	Arg	Ala	Arg	Pro	Gly	Gly	Ser	Arg	Ser	875	880	885
Arg	Asn	Trp	Ala	Glu	Leu	Ser	Asn	Arg	Lys	Pro	Ala	Pro			890	895	

<210> 13

<211> 631

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3473847CD1

<400> 13

Met	Phe	Leu	Leu	Ala	Trp	Gly	Gln	Asp	Pro	Trp	Arg	Leu	Pro	Gly	15
1				5					10						
Thr	Tyr	Val	Val	Val	Leu	Lys	Glu	Glu	Thr	His	Leu	Ser	Gln	Ser	30
				20					25						
Glu	Arg	Thr	Ala	Arg	Arg	Leu	Gln	Ala	Gln	Ala	Ala	Arg	Arg	Gly	45
				35					40						
Tyr	Leu	Thr	Lys	Ile	Leu	His	Val	Phe	His	Gly	Leu	Leu	Pro	Gly	60
				50					55						
Phe	Leu	Val	Lys	Met	Ser	Gly	Asp	Leu	Leu	Glu	Leu	Ala	Leu	Lys	75
				65					70						
Leu	Pro	His	Val	Asp	Tyr	Ile	Glu	Glu	Asp	Ser	Ser	Val	Phe	Ala	90
				80					85						
Gln	Ser	Ile	Pro	Trp	Asn	Leu	Glu	Arg	Ile	Thr	Pro	Pro	Arg	Tyr	105
				95					100						
Arg	Ala	Asp	Glu	Tyr	Gln	Pro	Pro	Asp	Gly	Gly	Ser	Leu	Val	Glu	120
				110					115						
Val	Tyr	Leu	Leu	Asp	Thr	Ser	Ile	Gln	Ser	Asp	His	Arg	Glu	Ile	135
				125					130						
Glu	Gly	Arg	Val	Met	Val	Thr	Asp	Phe	Glu	Asn	Val	Pro	Glu	Glu	150
				140					145						
Asp	Gly	Thr	Arg	Phe	His	Arg	Gln	Ala	Ser	Lys	Cys	Asp	Ser	His	165
				155					160						
Gly	Thr	His	Leu	Ala	Gly	Val	Val	Ser	Gly	Arg	Asp	Ala	Gly	Val	180
				170					175						
Ala	Lys	Gly	Ala	Ser	Met	Arg	Ser	Leu	Arg	Val	Leu	Asn	Cys	Gln	195
				185					190						
Gly	Lys	Gly	Thr	Val	Ser	Gly	Thr	Leu	Ile	Gly	Leu	Glu	Phe	Ile	210
				200					205						
Arg	Lys	Ser	Gln	Leu	Val	Gln	Pro	Val	Gly	Pro	Leu	Val	Val	Leu	225
				215					220						
Leu	Pro	Leu	Ala	Gly	Gly	Tyr	Ser	Arg	Val	Leu	Asn	Ala	Ala	Cys	240
				230					235						
Gln	Arg	Leu	Ala	Arg	Ala	Gly	Val	Val	Leu	Val	Thr	Ala	Ala	Gly	255
				245					250						
Asn	Phe	Arg	Asp	Asp	Ala	Cys	Leu	Tyr	Ser	Pro	Ala	Ser	Ala	Pro	270
				260					265						
Glu	Val	Ile	Thr	Val	Gly	Ala	Thr	Asn	Ala	Gln	Asp	Gln	Pro	Val	285
				275					280						
Thr	Leu	Gly	Thr	Leu	Gly	Thr	Asn	Phe	Gly	Arg	Cys	Val	Asp	Leu	300
				290					295						
Phe	Ala	Pro	Gly	Glu	Asp	Ile	Ile	Gly	Ala	Ser	Ser	Asp	Cys	Ser	315
				305					310						
Thr	Cys	Phe	Val	Ser	Gln	Ser	Gly	Thr	Ser	Gln	Ala	Ala	Ala	His	330
				320					325						
Val	Ala	Gly	Ile	Ala	Ala	Met	Met	Leu	Ser	Ala	Glu	Pro	Glu	Leu	345
				335					340						
Thr	Leu	Ala	Glu	Leu	Arg	Gln	Arg	Leu	Ile	His	Phe	Ser	Ala	Lys	360
				350					355						
Asp	Val	Ile	Asn	Glu	Ala	Trp	Phe	Pro	Glu	Asp	Gln	Arg	Val	Leu	375
				365					370						
Thr	Pro	Asn	Leu	Val	Ala	Ala	Leu	Pro	Pro	Ser	Thr	His	Gly	Ala	390
				380					385						
Gly	Trp	Gln	Leu	Phe	Cys	Arg	Thr	Val	Trp	Ser	Ala	His	Ser	Gly	405
				395					400						
Pro	Thr	Arg	Met	Ala	Thr	Ala	Ile	Ala	Arg	Cys	Ala	Pro	Asp	Glu	420
				410					415						
Glu	Leu	Leu	Ser	Cys	Ser	Ser	Phe	Ser	Arg	Ser	Gly	Lys	Arg	Arg	435
				425					430						
Gly	Glu	Arg	Met	Glu	Ala	Gln	Gly	Gly	Lys	Leu	Val	Cys	Arg	Ala	450
				440					445						
His	Asn	Ala	Phe	Gly	Gly	Glu	Gly	Val	Tyr	Ala	Ile	Ala	Arg	Cys	465
				455					460						
Cys	Leu	Leu	Pro	Gln	Ala	Asn	Cys	Ser	Val	His	Thr	Ala	Pro	Pro	480
				470					475						
Ala	Glu	Ala	Ser	Met	Gly	Thr	Arg	Val	His	Cys	His	Gln	Gln	Gly	495
				485					490						
His	Val	Leu	Thr	Gly	Cys	Ser	Ser	His	Trp	Glu	Val	Glu	Asp	Leu	

Gly Thr His Lys	500	Pro Pro Val Leu Arg	505	Pro Arg Gly Gln Pro	510
Gln Cys Val Gly	515	His Arg Glu Ala Ser	520	Ile His Ala Ser Cys	525
His Ala Pro Gly	530	Leu Glu Cys Lys Val	535	Lys Glu His Gly Ile	540
Ala Pro Gln Glu	545	Gln Val Thr Val Ala	550	Cys Glu Glu Gly Trp	555
Leu Thr Gly Cys	560	Ser Ala Leu Pro Gly	565	Thr Ser His Val Leu	570
Ala Tyr Ala Val	575	Asp Asn Thr Cys Val	580	Val Arg Ser Arg Asp	585
Ser Thr Thr Gly	590	Ser Thr Ser Glu Glu	595	Ala Val Thr Ala Val	600
Ile Cys Cys Arg	605	Ser Arg His Leu Ala	610	Gln Ala Ser Gln Glu	615
Gln	620		625		630

<210> 14

<211> 470

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 3750004CD1

<400> 14

Met Arg His Arg Thr	1	Asp Leu Gly Gln Asn	10	Leu Leu Leu Phe Leu	15
Trp Ala Leu Leu Asn	20	Cys Gly Leu Gly Val	25	Ser Ala Gln Gly Pro	30
Gly Glu Trp Thr Pro	35	Trp Val Ser Trp Thr	40	Arg Cys Ser Ser Ser	45
Cys Gly Arg Gly Val	50	Ser Val Arg Ser Arg	55	Arg Cys Leu Arg Leu	60
Pro Gly Glu Glu Pro	65	Cys Trp Gly Asp Ser	70	His Glu Tyr Arg Leu	75
Cys Gln Leu Pro Asp	80	Cys Pro Pro Gly Ala	85	Val Pro Phe Arg Asp	90
Leu Gln Cys Ala Leu	95	Tyr Asn Gly Arg Pro	100	Val Leu Gly Thr Gln	105
Lys Thr Tyr Gln Trp	110	Val Pro Phe His Gly	115	Ala Pro Asn Gln Cys	120
Asp Leu Asn Cys Leu	125	Ala Glu Gly His Ala	130	Phe Tyr His Ser Phe	135
Gly Arg Val Leu Asp	140	Gly Thr Ala Cys Ser	145	Pro Gly Ala Gln Gly	150
Val Cys Val Ala Gly	155	Arg Cys Leu Ser Ala	160	Gly Cys Asp Gly Leu	165
Leu Gly Ser Gly Ala	170	Leu Glu Asp Arg Cys	175	Gly Arg Cys Gly Gly	180
Ala Asn Asp Ser Cys	185	Leu Phe Val Gln Arg	190	Val Phe Arg Asp Ala	195
Gly Ala Phe Ala Gly	200	Tyr Trp Asn Val Thr	205	Leu Ile Pro Glu Gly	210
Ala Arg His Ile Arg	215	Val Glu His Arg Ser	220	Arg Asn His Leu Gly	225
Ile Leu Gly Ser Leu	230	Met Gly Gly Asp Gly	235	Arg Tyr Val Leu Asn	240
Gly His Trp Val Val	245	Ser Pro Pro Gly Thr	250	Tyr Glu Ala Ala Gly	255
Thr His Val Val Tyr	260	Thr Arg Asp Thr Gly	265	Pro Gln Glu Thr Leu	270
Gln Ala Ala Gly Pro		Thr Ser His Asp Leu		Leu Leu Gln Val Leu	

Leu Gln Glu Pro	275	280	285
Asn Pro Gly Ile Glu	290	Phe Glu Phe Trp Leu	Pro
Arg Glu Arg Tyr	305	Arg Val Gln Ala Leu	Gly
Trp Pro Leu Arg	320	Gly Val Glu Pro Gln	Pro
Pro Ala Ala Pro	335	Gln Thr Pro Thr Leu	Ala
Pro Asp Pro Cys	350	Thr Arg Gly Arg Ala	His
Arg Leu Leu His	365	Phe Val Phe Gln Ala	Arg
Val Leu Gly His	380	Glu Thr Arg Tyr Glu	Val
Arg Ile Gln Leu	395	Ser Pro Leu Arg Ala	Arg
Glu Tyr Val Trp	410	Pro Cys Pro Met Leu	Ala
Pro His Arg Asp	425	Gln Arg Leu Val Ser	Pro
Asp Gly Thr Gln	440	Pro His Ala Gly Tyr	Ala
Arg Pro Trp Ser	455	Arg Ile Arg Leu Thr	Ala
Arg Arg Cys Pro	470		

<210> 15
 <211> 110
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 4904126CD1

Met Ala Asp Lys Val	1	Leu Lys Glu Lys Arg	10	Lys Gln Phe Ile Arg	15
Ser Val Gly Glu Gly	20	Thr Ile Asn Gly Leu	25	Leu Gly Glu Leu Leu	30
Glu Thr Arg Val Leu	35	Ser Gln Glu Glu Ile	40	Glu Ile Val Lys Cys	45
Glu Asn Ala Thr Val	50	Met Asp Lys Ala Arg	55	Ala Leu Leu Asp Ser	60
Val Ile Arg Lys Gly	65	Ala Pro Ala Cys Gln	70	Ile Cys Ile Thr Tyr	75
Ile Cys Glu Glu Asp	80	Ser His Leu Ala Gly	85	Thr Leu Gly Leu Ser	90
Ala Gly Pro Thr Ser	95	Gly Asn His Leu Thr	100	Thr Gln Asp Ser Gln	105
Ile Val Leu Pro Ser	110				

<210> 16
 <211> 879
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 71268415CD1

Met Ser Leu Phe Ile	1	Phe Cys Arg Gln Leu	10	Phe Ala Pro Ser Tyr	15
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Thr Glu Thr His Tyr Thr Ser Ser Gly Asn Pro Gln Thr Thr Thr
 20 25 30
 Arg Lys Leu Glu Asp His Cys Phe Tyr His Gly Thr Val Arg Glu
 35 40 45
 Thr Glu Leu Ser Ser Val Thr Leu Ser Thr Cys Arg Gly Ile Arg
 50 55 60
 Gly Leu Ile Thr Val Ser Ser Asn Leu Ser Tyr Val Ile Glu Pro
 65 70 75
 Leu Pro Asp Ser Lys Gly Gln His Leu Ile Tyr Arg Ser Glu His
 80 85 90
 Leu Lys Pro Pro Pro Gly Asn Cys Gly Phe Glu His Ser Lys Pro
 95 100 105
 Thr Thr Arg Asp Trp Ala Leu Gln Phe Thr Gln Gln Thr Lys Lys
 110 115 120
 Arg Pro Arg Arg Met Lys Arg Glu Asp Leu Asn Ser Met Lys Tyr
 125 130 135
 Val Glu Leu Tyr Leu Val Ala Asp Tyr Leu Glu Phe Gln Lys Asn
 140 145 150
 Arg Arg Asp Gln Asp Ala Thr Lys His Lys Leu Ile Glu Ile Ala
 155 160 165
 Asn Tyr Val Asp Lys Phe Tyr Arg Ser Leu Asn Ile Arg Ile Ala
 170 175 180
 Leu Val Gly Leu Glu Val Trp Thr His Gly Asn Met Cys Glu Val
 185 190 195
 Ser Glu Asn Pro Tyr Ser Thr Leu Trp Ser Phe Leu Ser Trp Arg
 200 205 210
 Arg Lys Leu Leu Ala Gln Lys Tyr His Asp Asn Ala Gln Leu Ile
 215 220 225
 Thr Gly Met Ser Phe His Gly Thr Thr Ile Gly Leu Ala Pro Leu
 230 235 240
 Met Ala Met Cys Ser Val Tyr Gln Ser Gly Gly Val Asn Met Asp
 245 250 255
 His Ser Glu Asn Ala Ile Gly Val Ala Ala Thr Met Ala His Glu
 260 265 270
 Met Gly His Asn Phe Gly Met Thr His Asp Ser Ala Asp Cys Cys
 275 280 285
 Ser Ala Ser Ala Ala Asp Gly Gly Cys Ile Met Ala Ala Ala Thr
 290 295 300
 Gly His Pro Phe Pro Lys Val Phe Asn Gly Cys Asn Arg Arg Glu
 305 310 315
 Leu Asp Arg Tyr Leu Gln Ser Gly Gly Gly Met Cys Leu Ser Asn
 320 325 330
 Met Pro Asp Thr Arg Met Leu Tyr Gly Gly Arg Arg Cys Gly Asn
 335 340 345
 Gly Tyr Leu Glu Asp Gly Glu Glu Cys Asp Cys Gly Glu Glu Glu
 350 355 360
 Glu Cys Asn Asn Pro Cys Cys Asn Ala Ser Asn Cys Thr Leu Arg
 365 370 375
 Pro Gly Ala Glu Cys Ala His Gly Ser Cys Cys His Gln Cys Lys
 380 385 390
 Leu Leu Ala Pro Gly Thr Leu Cys Arg Glu Gln Ala Arg Gln Cys
 395 400 405
 Asp Leu Pro Glu Phe Cys Thr Gly Lys Ser Pro His Cys Pro Thr
 410 415 420
 Asn Phe Tyr Gln Met Asp Gly Thr Pro Cys Glu Gly Gly Gln Ala
 425 430 435
 Tyr Cys Tyr Asn Gly Met Cys Leu Thr Tyr Gln Glu Gln Cys Gln
 440 445 450
 Gln Leu Trp Gly Pro Gly Ala Arg Pro Ala Pro Asp Leu Cys Phe
 455 460 465
 Glu Lys Val Asn Val Ala Gly Asp Thr Phe Gly Asn Cys Gly Lys
 470 475 480
 Asp Met Asn Gly Glu His Arg Lys Cys Asn Met Arg Asp Ala Lys
 485 490 495
 Cys Gly Lys Ile Gln Cys Gln Ser Ser Glu Ala Arg Pro Leu Glu
 500 505 510
 Ser Asn Ala Val Pro Ile Asp Thr Thr Ile Ile Met Asn Gly Arg

Gln Ile Gln Cys	Arg Gly Thr His Val	Tyr Arg Gly Pro Glu	Glu
515	520	525	
530	535	540	
Glu Gly Asp Met	Leu Asp Pro Gly Leu	Val Met Thr Gly Thr	Lys
545	550	555	
Cys Gly Tyr Asn	His Ile Cys Phe Glu	Gly Gln Cys Arg Asn	Thr
560	565	570	
Ser Phe Phe Glu	Thr Glu Gly Cys Gly	Lys Lys Cys Asn Gly	His
575	580	585	
Gly Val Cys Asn	Asn Asn Gln Asn Cys	His Cys Leu Pro Gly	Trp
590	595	600	
Ala Pro Pro Phe	Cys Asn Thr Pro Gly	His Gly Gly Ser Ile	Asp
605	610	615	
Ser Gly Pro Met	Pro Pro Glu Ser Val	Gly Pro Val Val Ala	Gly
620	625	630	
Val Leu Val Ala	Ile Leu Val Leu Ala	Val Leu Met Leu Met	Tyr
635	640	645	
Tyr Cys Cys Arg	Gln Asn Asn Lys Leu	Gly Gln Leu Lys Pro	Ser
650	655	660	
Ala Leu Pro Ser	Lys Leu Arg Gln Gln	Phe Ser Cys Pro Phe	Arg
665	670	675	
Val Ser Gln Asn	Ser Gly Thr Gly His	Ala Asn Pro Thr Phe	Lys
680	685	690	
Leu Gln Thr Pro	Gln Gly Lys Arg Lys	Val Ile Asn Thr Pro	Glu
695	700	705	
Ile Leu Arg Lys	Pro Ser Gln Pro Pro	Pro Arg Pro Pro Pro	Asp
710	715	720	
Tyr Leu Arg Gly	Gly Ser Pro Pro Ala	Pro Leu Pro Ala His	Leu
725	730	735	
Ser Arg Ala Ala	Arg Asn Ser Pro Gly	Pro Gly Ser Gln Ile	Glu
740	745	750	
Arg Thr Glu Ser	Ser Arg Arg Pro Pro	Pro Ser Arg Pro Ile	Pro
755	760	765	
Pro Ala Pro Asn	Cys Ile Val Ser Gln	Asp Phe Ser Arg Pro	Arg
770	775	780	
Pro Pro Gln Lys	Ala Leu Pro Ala Asn	Pro Val Pro Gly Arg	Arg
785	790	795	
Ser Leu Pro Arg	Pro Gly Gly Ala Ser	Pro Leu Arg Pro Pro	Gly
800	805	810	
Ala Gly Pro Gln	Gln Ser Arg Pro Leu	Ala Ala Leu Ala Pro	Lys
815	820	825	
Val Ser Pro Arg	Glu Ala Leu Lys Val	Lys Ala Gly Thr Arg	Gly
830	835	840	
Leu Gln Gly Gly	Arg Cys Arg Val Glu	Lys Thr Lys Gln Phe	Met
845	850	855	
Leu Leu Val Val	Trp Thr Glu Leu Pro	Glu Gln Lys Pro Arg	Ala
860	865	870	
Lys His Ser Cys	Phe Leu Val Pro Ala		
875			

<210> 17

<211> 850

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7473301CD1

<400> 17

Met Asp Lys Glu Asn	Ser Asp Val Ser	Ala Ala Pro Ala Asp	Leu
1	5	10	15
Lys Ile Ser Asn Ile	Ser Val Gln Val	Ser Ala Gln Lys	Lys
20	25	30	
Leu Pro Val Arg Arg	Pro Pro Leu Pro	Gly Arg Arg Leu Pro	Leu
35	40	45	
Pro Gly Arg Arg Pro	Pro Gln Arg Pro	Ile Gly Lys Ala Lys	Pro

Lys Lys Gln Ser	50	Lys Lys Val Pro	55	Phe Trp Asn Val Gln Asn	60
Lys Ile Ile Leu	65	Phe Thr Val Phe Leu	70	Phe Ile Leu Ala Val Ile	75
Ala Trp Thr Leu	80	Leu Trp Leu Tyr Ile	85	Ser Lys Thr Glu Ser Lys	90
Asp Ala Phe Tyr	95	Phe Ala Gly Met Phe	100	Arg Ile Thr Asn Ile Glu	105
Phe Leu Pro Glu	110	Tyr Arg Gln Lys Glu	115	Ser Arg Glu Phe Leu Ser	120
Val Ser Arg Thr	125	Val Gln Gln Val Ile	130	Asn Leu Val Tyr Thr Thr	135
Ser Ala Phe Ser	140	Lys Phe Tyr Glu Gln	145	Ser Val Val Ala Asp Val	150
Ser Ser Asn Asn	155	Lys Gly Gly Leu Leu	160	Val His Phe Trp Ile Val	165
Phe Val Met Pro	170	Arg Ala Lys Gly His	175	Ile Phe Cys Glu Asp Cys	180
Val Ala Ala Ile	185	Leu Lys Asp Ser Ile	190	Gln Thr Ser Ile Ile Asn	195
Arg Thr Ser Val	200	Gly Ser Leu Gln Gly	205	Leu Ala Val Asp Met Asp	210
Ser Val Val Leu	215	Asn Gly Asp Cys Trp	220	Ser Phe Leu Lys Lys Lys	225
Lys Arg Lys Glu	230	Asn Gly Ala Val Ser	235	Thr Asp Lys Gly Cys Ser	240
Gln Tyr Phe Tyr	245	Ala Glu His Leu Ser	250	Leu His Tyr Pro Leu Glu	255
Ile Ser Ala Ala	260	Ser Gly Arg Leu Met	265	Cys His Phe Lys Leu Val	270
Ala Ile Val Gly	275	Tyr Leu Ile Arg Leu	280	Ser Ile Lys Ser Ile Gln	285
Ile Glu Ala Asp	290	Asn Cys Val Thr Asp	295	Ser Leu Thr Ile Tyr Asp	300
Ser Leu Leu Pro	305	Ile Arg Ser Ser Ile	310	Leu Tyr Arg Ile Cys Glu	315
Pro Thr Arg Thr	320	Leu Met Ser Phe Val	325	Ser Thr Asn Asn Leu Met	330
Leu Val Thr Phe	335	Lys Ser Pro His Ile	340	Arg Arg Leu Ser Gly Ile	345
Arg Ala Tyr Phe	350	Glu Val Ile Pro Glu	355	Gln Lys Cys Glu Asn Thr	360
Val Leu Val Lys	365	Asp Ile Thr Gly Phe	370	Glu Gly Lys Ile Ser Ser	375
Pro Tyr Tyr Pro	380	Ser Tyr Tyr Pro Pro	385	Lys Cys Lys Cys Thr Trp	390
Lys Phe Gln Thr	395	Ser Leu Ser Thr Leu	400	Gly Ile Ala Leu Lys Phe	405
Tyr Asn Tyr Ser	410	Ile Thr Lys Lys Ser	415	Met Lys Gly Cys Glu His	420
Gly Trp Trp Glu	425	Ile Tyr Glu His Met	430	Tyr Cys Gly Ser Tyr Met	435
Asp His Gln Thr	440	Ile Phe Arg Val Pro	445	Ser Pro Leu Val His Ile	450
Gln Leu Gln Cys	455	Ser Ser Arg Leu Ser	460	Gly Lys Pro Leu Leu Ala	465
Glu Tyr Gly Ser	470	Tyr Asn Ile Ser Gln	475	Pro Cys Pro Val Gly Ser	480
Phe Arg Cys Ser	485	Ser Gly Leu Cys Val	490	Pro Gln Ala Gln Arg Gly	495
Asp Gly Val Asn	500	Asp Cys Phe Asp Glu	505	Ser Asp Glu Leu Phe Cys	510
Val Ser Pro Gln	515	Pro Ala Cys Asn Thr	520	Ser Ser Phe Arg Gln His	525
Gly Pro Leu Ile	530	Cys Asp Gly Phe Arg	535	Asp Cys Glu Asn Gly Arg	540
	545		550		555

Asp	Glu	Gln	Asn	Cys	Thr	Gln	Ser	Ile	Pro	Cys	Asn	Asn	Arg	Thr
				560					565					570
Phe	Lys	Cys	Gly	Asn	Asp	Ile	Cys	Phe	Arg	Lys	Gln	Asn	Ala	Lys
				575					580					585
Cys	Asp	Gly	Thr	Val	Asp	Cys	Pro	Asp	Gly	Ser	Asp	Glu	Glu	Gly
				590					595					600
Cys	Thr	Cys	Ser	Arg	Ser	Ser	Ser	Ala	Leu	His	Arg	Ile	Ile	Gly
				605					610					615
Gly	Thr	Asp	Thr	Leu	Glu	Gly	Gly	Trp	Pro	Trp	Gln	Val	Ser	Leu
				620					625					630
His	Phe	Val	Gly	Ser	Ala	Tyr	Cys	Gly	Ala	Ser	Val	Ile	Ser	Arg
				635					640					645
Glu	Trp	Leu	Leu	Ser	Ala	Ala	His	Cys	Phe	His	Gly	Asn	Arg	Leu
				650					655					660
Ser	Asp	Pro	Thr	Pro	Trp	Thr	Ala	His	Leu	Gly	Met	Tyr	Val	Gln
				665					670					675
Gly	Asn	Ala	Lys	Phe	Val	Ser	Pro	Val	Arg	Arg	Ile	Val	Val	His
				680					685					690
Glu	Tyr	Tyr	Asn	Ser	Gln	Thr	Phe	Asp	Tyr	Asp	Ile	Ala	Leu	Leu
				695					700					705
Gln	Leu	Ser	Ile	Ala	Trp	Pro	Glu	Thr	Leu	Lys	Gln	Leu	Ile	Gln
				710					715					720
Pro	Ile	Cys	Ile	Pro	Pro	Thr	Gly	Gln	Arg	Val	Arg	Ser	Gly	Glu
				725					730					735
Lys	Cys	Trp	Val	Thr	Gly	Trp	Gly	Arg	Arg	His	Glu	Ala	Asp	Asn
				740					745					750
Lys	Gly	Ser	Leu	Val	Leu	Gln	Gln	Ala	Glu	Val	Glu	Leu	Ile	Asp
				755					760					765
Gln	Thr	Leu	Cys	Val	Ser	Thr	Tyr	Gly	Ile	Ile	Thr	Ser	Arg	Met
				770					775					780
Leu	Cys	Ala	Gly	Ile	Met	Ser	Gly	Lys	Arg	Asp	Ala	Cys	Lys	Gly
				785					790					795
Asp	Ser	Gly	Gly	Pro	Leu	Ser	Cys	Arg	Arg	Lys	Ser	Asp	Gly	Lys
				800					805					810
Trp	Ile	Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	His	Gly	Cys	Gly	Arg
				815					820					825
Pro	Asn	Phe	Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser	Asn	Phe	Val	Pro
				830					835					840
Trp	Ile	His	Lys	Tyr	Val	Pro	Ser	Leu	Leu					
				845					850					

<210> 18

<211> 254

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7473308CD1

<400> 18

Met	Gln	Asp	His	Arg	Lys	Gly	Lys	Ala	Ala	Val	Gly	Val	Ser	Phe
1				5					10					15
Asp	Asp	Asp	Asp	Lys	Ile	Val	Gly	Gly	Tyr	Asn	Cys	Glu	Glu	Asn
				20					25					30
Ser	Val	Pro	Tyr	Gln	Val	Ser	Leu	Asn	Ser	Gly	Tyr	His	Phe	Cys
				35					40					45
Val	Gly	Ser	Leu	Asn	Arg	Glu	Tyr	Cys	Ile	Gln	Val	Arg	Leu	Gly
				50					55					60
Glu	His	Asn	Ile	Glu	Val	Leu	Glu	Gly	Asn	Glu	Gln	Phe	Ile	Tyr
				65					70					75
Ala	Val	Lys	Ile	Ile	Arg	His	Pro	Lys	Tyr	Asn	Ser	Trp	Thr	Leu
				80					85					90
Asp	Asn	Asp	Ile	Leu	Leu	Ile	Lys	Leu	Ser	Thr	Pro	Ala	Ile	Ile
				95					100					105
Asn	Ala	His	Val	Ser	Thr	Ile	Ser	Leu	Pro	Thr	Thr	Pro	Pro	Ala
				110					115					120

Ala Gly Thr Glu Cys	Leu Ile Ser Gly	Trp Gly Asn Thr Leu Ser	
125		130	135
Ser Gly Ala Asp Tyr	Pro Asp Glu Leu	Gln Cys Leu Asp Ala Pro	
140		145	150
Val Leu Ser Gln Ala	Glu Tyr Glu Ala	Ser Tyr Pro Gly Lys Ile	
155		160	165
Thr Asn Asn Val Phe	Cys Val Gly Phe	Leu Glu Gly Gly Lys Asp	
170		175	180
Ser Cys Gln Ile Ile	Pro Ile Lys Val	Gln Gln Leu Val Thr Ser	
185		190	195
Ser Gln Glu Thr Asp	Ile Arg Ile Pro	Met Ala Leu Gln Thr Ala	
200		205	210
Ala Ser Thr Ser Tyr	Leu Gly Pro Leu	Asp Ser Leu His Arg Lys	
215		220	225
Val Ser His Pro Thr	Glu Lys Arg Cys	Gln Gln Lys Gln Gly Met	
230		235	240
Lys Ile Thr Asp Asn	His Gly Ile Thr	Ser Lys Trp Ser Val	
245		250	

<210> 19

<211> 568

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7478021CD1

<400> 19

Met Leu Ala Ala Ser	Ile Phe Arg Pro	Thr Leu Leu Leu Cys	Trp
1	5	10	15
Leu Ala Ala Pro Trp	Pro Thr Gln Pro	Glu Ser Leu Phe His	Ser
20		25	30
Arg Asp Arg Ser Asp	Leu Glu Pro Ser	Pro Leu Arg Gln Ala	Lys
35		40	45
Pro Ile Ala Asp Leu	His Ala Ala Gln	Arg Phe Leu Ser Arg	Tyr
50		55	60
Gly Trp Ser Gly Val	Trp Ala Ala Trp	Gly Pro Ser Pro Glu	Gly
65		70	75
Pro Pro Glu Thr Pro	Lys Gly Ala Ala	Leu Ala Glu Ala Val	Arg
80		85	90
Arg Phe Gln Arg Ala	Asn Ala Leu Pro	Ala Ser Gly Glu Leu	Asp
95		100	105
Ala Ala Thr Leu Ala	Ala Met Asn Arg	Pro Arg Cys Gly Val	Pro
110		115	120
Asp Met Arg Pro Pro	Pro Pro Ser Ala	Pro Pro Ser Pro Pro	Gly
125		130	135
Pro Pro Pro Arg Ala	Arg Ser Arg Arg	Ser Pro Arg Ala Pro	Leu
140		145	150
Ser Leu Ser Arg Arg	Gly Trp Gln Pro	Arg Gly Tyr Pro Asp	Gly
155		160	165
Gly Ala Ala Gln Ala	Phe Ser Lys Arg	Thr Leu Ser Trp Arg	Leu
170		175	180
Leu Gly Glu Ala Leu	Ser Ser Gln Leu	Ser Val Ala Asp Gln	Arg
185		190	195
Arg Ile Glu Ala Leu	Ala Phe Arg Met	Trp Ser Glu Val Thr	Pro
200		205	210
Leu Asp Phe Arg Glu	Asp Leu Ala Ala	Pro Gly Ala Ala Val	Asp
215		220	225
Ile Lys Leu Gly Phe	Gly Arg Arg His	Leu Gly Cys Pro Arg	Ala
230		235	240
Phe Asp Gly Ser Gly	Gln Glu Phe Ala	His Ala Trp Arg Leu	Gly
245		250	255
Asp Ile His Phe Asp	Asp Asp Glu His	Phe Thr Pro Pro Thr	Ser
260		265	270
Asp Thr Gly Ile Ser	Leu Leu Lys Val	Ala Val His Glu Ile	Gly
275		280	285

His Val Leu Gly	Leu Pro His Thr Tyr	Arg Thr Gly Ser Ile	Met
290	295		300
Gln Pro Asn Tyr	Ile Pro Gln Glu Pro	Ala Phe Glu Leu Asp	Trp
305	310		315
Ser Asp Arg Lys	Ala Ile Gln Lys Leu	Tyr Gly Ser Cys Glu	Gly
320	325		330
Ser Phe Asp Thr	Ala Phe Asp Trp Ile	Arg Lys Glu Arg Asn	Gln
335	340		345
Tyr Gly Glu Val	Met Val Arg Phe Ser	Thr Tyr Phe Phe Arg	Asn
350	355		360
Ser Trp Tyr Trp	Leu Tyr Glu Asn Arg	Asn Asn Arg Thr Arg	Tyr
365	370		375
Gly Asp Pro Ile	Gln Ile Leu Thr Gly	Trp Pro Gly Ile Pro	Thr
380	385		390
His Asn Ile Asp	Ala Phe Val His Ile	Trp Thr Trp Lys Arg	Asp
395	400		405
Glu Arg Tyr Phe	Phe Gln Gly Asn Gln	Tyr Trp Arg Tyr Asp	Ser
410	415		420
Asp Lys Asp Gln	Ala Leu Thr Glu Asp	Glu Gln Gly Lys Ser	Tyr
425	430		435
Pro Lys Leu Ile	Ser Glu Gly Phe Pro	Gly Ile Pro Ser Pro	Leu
440	445		450
Asp Thr Ala Phe	Tyr Asp Arg Arg Gln	Lys Leu Ile Tyr Phe	Phe
455	460		465
Lys Glu Ser Leu	Val Phe Ala Phe Asp	Val Asn Arg Asn Arg	Val
470	475		480
Leu Asn Ser Tyr	Pro Lys Arg Ile Thr	Glu Val Phe Pro Ala	Val
485	490		495
Ile Pro Gln Asn	His Pro Phe Arg Asn	Ile Asp Ser Ala Tyr	Tyr
500	505		510
Ser Tyr Ala Tyr	Asn Ser Ile Phe Phe	Phe Lys Gly Asn Ala	Tyr
515	520		525
Trp Lys Val Val	Asn Asp Lys Asp Lys	Gln Gln Asn Ser Trp	Leu
530	535		540
Pro Ala Asn Gly	Leu Phe Pro Lys Lys	Phe Ile Ser Glu Lys	Trp
545	550		555
Phe Asp Val Cys	Asp Val His Ile Ser	Thr Leu Asn Met	
560	565		

<210> 20

<211> 306

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 4333459CD1

<400> 20

Met Ser Leu Lys	Met Leu Ile Ser Arg	Asn Lys Leu Ile Leu	Leu
1	5	10	15
Leu Gly Ile Val	Phe Phe Glu Arg Gly	Lys Ser Ala Thr Leu	Ser
20	25		30
Leu Pro Lys Ala	Pro Ser Cys Gly Gln	Ser Leu Val Lys Val	Gln
35	40		45
Pro Trp Asn Tyr	Phe Asn Ile Phe Ser	Arg Ile Leu Gly Gly	Ser
50	55		60
Gln Val Glu Lys	Gly Ser Tyr Pro Trp	Gln Val Ser Leu Lys	Gln
65	70		75
Arg Gln Lys His	Ile Cys Gly Gly Ser	Ile Val Ser Pro Gln	Trp
80	85		90
Val Ile Thr Ala	Ala His Cys Ile Ala	Asn Arg Asn Ile Val	Ser
95	100		105
Thr Leu Asn Val	Thr Ala Gly Glu Tyr	Asp Leu Ser Gln Thr	Asp
110	115		120
Pro Gly Glu Gln	Thr Leu Thr Ile Glu	Thr Val Ile Ile His	Pro
125	130		135

His Phe Ser Thr Lys Lys Pro Met Asp Tyr Asp Ile Ala Leu Leu
 140 145 150
 Lys Met Ala Gly Ala Phe Gln Phe Gly His Phe Val Gly Pro Ile
 155 160 165
 Cys Leu Pro Glu Leu Arg Glu Gln Phe Glu Ala Gly Phe Ile Cys
 170 175 180
 Thr Thr Ala Gly Trp Gly Arg Leu Thr Glu Gly Gly Val Leu Ser
 185 190 195
 Gln Val Leu Gln Glu Val Asn Leu Pro Ile Leu Thr Trp Glu Glu
 200 205 210
 Cys Val Ala Ala Leu Leu Thr Leu Lys Arg Pro Ile Ser Gly Lys
 215 220 225
 Thr Phe Leu Cys Thr Gly Phe Pro Asp Gly Gly Arg Asp Ala Cys
 230 235 240
 Gln Gly Asp Ser Gly Gly Ser Leu Met Cys Arg Asn Lys Lys Gly
 245 250 255
 Ala Trp Thr Leu Ala Gly Val Thr Ser Trp Gly Leu Gly Cys Gly
 260 265 270
 Arg Gly Trp Arg Asn Asn Val Arg Lys Ser Asp Gln Gly Ser Pro
 275 280 285
 Gly Ile Phe Thr Asp Ile Ser Lys Val Leu Ser Trp Ile His Glu
 290 295 300
 His Ile Gln Thr Gly Asn
 305

<210> 21
 <211> 953
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 6817347CD1

<400> 21
 Met Thr Leu Leu Ala Pro Trp Tyr Thr Gly Pro Met Ile Pro Met
 1 5 10 15
 Asp Val Asn Glu Pro Ser Ser Val Thr Thr Ala Pro Thr Leu Ser
 20 25 30
 Ser Ser Leu Gln His Ile Ser Ser Phe Leu Ala Thr Gly Lys Lys
 35 40 45
 Leu Ser Leu His Phe Gly His Pro Arg Glu Cys Glu Val Thr Arg
 50 55 60
 Ile Asp Asp Lys Asn Arg Arg Gly Leu Glu Asp Ser Glu Pro Gly
 65 70 75
 Ala Lys Leu Phe Asn Asn Asp Gly Val Cys Cys Cys Leu Gln Lys
 80 85 90
 Arg Gly Pro Val Asn Ile Thr Ser Val Cys Val Ser Pro Arg Thr
 95 100 105
 Leu Gln Ile Ser Val Phe Val Leu Ser Glu Lys Tyr Glu Gly Ile
 110 115 120
 Val Lys Phe Glu Ser Asp Glu Leu Pro Phe Gly Val Ile Gly Ser
 125 130 135
 Asn Ile Gly Asp Ala His Phe Gln Glu Phe Arg Ala Gly Ile Ser
 140 145 150
 Trp Lys Pro Val Val Asp Pro Asp Asp Pro Ile Pro Gln Phe Pro
 155 160 165
 Asp Cys Cys Ser Ser Ser Ser Ser Arg Ile Pro Ser Val Ser Val
 170 175 180
 Leu Val Ala Val Pro Leu Val Ala Gly His Lys Gly Gln Ala Phe
 185 190 195
 Ile Glu Arg Met Leu Gly Cys Phe Lys Glu Leu Lys Gln Glu Leu
 200 205 210
 Thr Gln Glu Gly Pro Gly Gly Gly His Pro Arg Ser Ala Trp Pro
 215 220 225
 Pro Arg Arg His Ala Gln Trp Pro Pro Glu Pro Cys Glu Gln Gly
 230 235 240

Glu	Glu	Pro	Pro	Pro	Val	Glu	Ala	Glu	Glu	Val	Glu	Glu	Ala	Glu	245	250
Thr	Ala	Glu	Lys	Ala	Glu	Arg	Lys	Val	Glu	Ala	Glu	Ala	Lys	Val	260	265
Glu	Gly	Lys	Ala	Glu	Ala	Ala	Gly	Lys	Ala	Glu	Ala	Ala	Gly	Lys	275	280
Val	Asp	Ala	Thr	Glu	Lys	Val	Glu	Thr	Ala	Gly	Lys	Val	Asp	Ala	290	295
Ala	Gly	Lys	Val	Glu	Thr	Ala	Glu	Gly	Pro	Gly	Arg	Arg	Ala	Glu	305	310
Leu	Lys	Leu	Glu	Pro	Glu	Pro	Glu	Pro	Val	Arg	Glu	Ala	Glu	Gln	320	325
Glu	Pro	Lys	Gln	Glu	Leu	Glu	Asp	Glu	Asn	Pro	Ala	Arg	Ser	Gly	335	340
Gly	Gly	Gly	Asn	Ser	Asp	Glu	Val	Pro	Pro	Pro	Thr	Leu	Pro	Ser	350	355
Asp	Pro	Pro	Arg	Pro	Pro	Asp	Pro	Ser	Pro	Arg	Arg	Ser	Arg	Ala	365	370
Pro	Arg	Arg	Arg	Pro	Arg	Pro	Arg	Pro	Gln	Thr	Arg	Leu	Arg	Thr	380	385
Pro	Pro	Gln	Pro	Arg	Pro	Arg	Pro	Pro	Pro	Arg	Pro	Arg	Pro	Arg	395	400
Arg	Gly	Pro	Gly	Gly	Gly	Cys	Leu	Asp	Val	Asp	Phe	Ala	Val	Gly	410	415
Pro	Pro	Gly	Cys	Ser	His	Val	Asn	Ser	Phe	Lys	Val	Gly	Glu	Asn	425	430
Trp	Arg	Gln	Glu	Leu	Arg	Val	Ile	Tyr	Gln	Cys	Phe	Val	Trp	Cys	440	445
Gly	Thr	Pro	Glu	Thr	Arg	Lys	Ser	Lys	Ala	Lys	Ser	Cys	Ile	Cys	455	460
His	Val	Cys	Gly	Thr	His	Leu	Asn	Arg	Leu	His	Ser	Cys	Leu	Ser	470	475
Cys	Val	Phe	Phe	Gly	Cys	Phe	Thr	Glu	Lys	His	Ile	His	Glu	His	485	490
Ala	Glu	Thr	Lys	Gln	His	Asn	Leu	Ala	Val	Asp	Leu	Tyr	Tyr	Gly	500	505
Gly	Ile	Tyr	Cys	Phe	Met	Cys	Lys	Asp	Tyr	Val	Tyr	Asp	Lys	Asp	515	520
Ile	Glu	Gln	Ile	Ala	Lys	Glu	Glu	Gln	Gly	Glu	Ala	Leu	Lys	Leu	530	535
Gln	Ala	Ser	Thr	Ser	Thr	Glu	Val	Ser	His	Gln	Gln	Cys	Ser	Val	545	550
Pro	Gly	Leu	Gly	Glu	Lys	Phe	Pro	Thr	Trp	Glu	Thr	Thr	Lys	Pro	560	565
Glu	Leu	Glu	Leu	Leu	Gly	His	Asn	Pro	Arg	Arg	Arg	Arg	Ile	Thr	575	580
Ser	Ser	Phe	Thr	Ile	Gly	Leu	Arg	Gly	Leu	Ile	Asn	Leu	Gly	Asn	590	595
Thr	Cys	Phe	Met	Asn	Cys	Ile	Val	Gln	Ala	Leu	Thr	His	Thr	Pro	605	610
Ile	Leu	Arg	Asp	Phe	Phe	Leu	Ser	Asp	Arg	His	Arg	Cys	Glu	Met	620	625
Pro	Ser	Pro	Glu	Leu	Cys	Leu	Val	Cys	Glu	Met	Ser	Ser	Leu	Phe	635	640
Arg	Glu	Leu	Tyr	Ser	Gly	Asn	Pro	Ser	Pro	His	Val	Pro	Tyr	Lys	650	655
Leu	Leu	His	Leu	Val	Trp	Ile	His	Ala	Arg	His	Leu	Ala	Gly	Tyr	665	670
Arg	Gln	Gln	Asp	Ala	His	Glu	Phe	Leu	Ile	Ala	Ala	Leu	Asp	Val	680	685
Leu	His	Arg	His	Cys	Lys	Gly	Asp	Asp	Val	Gly	Lys	Ala	Ala	Asn	695	700
Asn	Pro	Asn	His	Cys	Asn	Cys	Ile	Ile	Asp	Gln	Ile	Phe	Thr	Gly	710	715
Gly	Leu	Gln	Ser	Asp	Val	Thr	Cys	Gln	Ala	Cys	His	Gly	Val	Ser	725	730
Thr	Thr	Ile	Asp	Pro	Cys	Trp	Asp	Ile	Ser	Leu	Asp	Leu	Pro	Gly	735	

Ser Cys Thr Ser	740	Trp Pro Met Ser	745	Pro Gly Arg Glu Ser	750
Val Asn Gly Glu	755	His Ile Pro Gly	760	Ile Thr Thr Leu Thr	765
Cys Leu Arg Arg	770	Thr Arg Pro Glu	775	His Leu Gly Ser Ser	780
Lys Ile Lys Cys	785	Gly Ser Cys Gln Ser	790	Tyr Gln Glu Ser Thr	795
Gln Leu Thr Met	800	Asn Lys Leu Pro Val	805	Val Ala Cys Phe His	810
Lys Arg Phe Glu	815	His Ser Ala Lys Gln	820	Arg Arg Lys Ile Thr	825
Tyr Ile Ser Phe	830	Pro Leu Glu Leu Asp	835	Met Thr Pro Phe Met	840
Ser Ser Lys Glu	845	Arg Met Asn Gly	850	Gln Leu Gln Leu Pro	855
Asn Ser Gly Asn	860	Asn Glu Asn Lys Tyr	865	Ser Leu Phe Ala Val	870
Asn His Gln Gly	875	Thr Leu Glu Ser Gly	880	His Tyr Thr Ser Phe	885
Arg His His Lys	890	Asp Gln Trp Phe Lys	895	Cys Asp Asp Ala Val	900
Thr Lys Ala Ser	905	Ile Lys Asp Val Leu	910	Asp Ser Glu Gly Tyr	915
Leu Phe Tyr His	920	Lys Gln Val Leu Glu	925	His Glu Ser Glu Lys	930
Lys Glu Met Asn	935	Thr Gln Ala Tyr	940		945
	950				

<210> .22

<211> 2204

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 275791CB1

<400> 22

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gagcttttagc	agctgtcttg	gagataagta	agagagatgc	ttcaccatct	ctgagtcattg	120
aagatgatga	taagccaact	agcagcccag	ataccggatt	tgacagaagat	gatattcaag	180
aatgcccga	aaatccagac	actatggaaa	ctgagaagcc	caaaacaatc	acagagctgg	240
atcctgccag	ttttactgag	ataactaaag	actgtgatga	gaataaagaa	aacaaaactc	300
cagaaggatc	tcaggagaga	gttgattggc	tccagcagta	tgatatggag	cgtgaaaggg	360
aagagcaaga	gcttcagcag	gcactggctc	agagccttca	agagcaagag	gcttgggaac	420
agaaagaaga	tgatgacctc	aaaagagcta	ccgagttaag	tcttcaagag	tttaacaact	480
cctttgtgga	tgcatggggt	tctgatgagg	actctggaaa	tgaggatggt	tttgatatgg	540
agtacacaga	agctgaagct	gaggaactga	aaagaaatgc	tgagacagga	aatctgcctc	600
attcgtaccg	gctcatcagt	gttgtcagtc	acattggtag	cacttcttct	tcaggtcatt	660
acattagtga	tgtatatgac	attaagaagc	aagcgtgggt	tacttacaat	gacctggagg	720
tatcaaaaat	ccaagaggct	gccgtgcaga	gtgatcgaga	tcggagtggc	tacatcttct	780
tttatatgca	caaggagatc	tttgatgagc	tgctggaaac	agaaaagaac	tctcagtcac	840
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<220>

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The following are the names of the persons who have been
 appointed to the various positions in the office of the
 Secretary of the State, under the provisions of the
 Act of March 1st, 1870, relating to the organization
 of the Department of the Interior.
 The following are the names of the persons who have been
 appointed to the various positions in the office of the
 Secretary of the State, under the provisions of the
 Act of March 1st, 1870, relating to the organization
 of the Department of the Interior.